United States Department of Agriculture
Agricultural Research Service
Animal Husbandry Research Division
Dairy Cattle Research Branch

Symposium
on
Estimating Breeding Values of Dairy Sires and Cows

National Arboretum
Washington, D. C.
September 12-13, 1966

400620

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Introduction

OPENING REMARKS

E. L. Corley[a]

THE CHAIRMAN: It is with pleasure that I extend to you welcome to this Symposium and Workshop which we are designating the NATIONAL TECHNICAL SYMPOSIUM AND WORKSHOP ON ESTIMATING BREEDING VALUE OF DAIRY SIRES AND COWS. The presence of each of you here this morning bears testimony to the importance of this topic and to your desire to contribute to our knowledge of this problem area.

To officially welcome you to the Washington, D. C. I am privileged to be able to call upon the Director of the Animal Husbandry Research Division, Beltsville, Maryland. Most of you have known Dr. Hodgson and therefore, an introduction is hardly necessary. You may not be aware of the fact that he has given a lot of leadership to DHIA and to the National Cooperative Dairy Herd Improvement Program over a number of years. For example, during the 1950's, when it was quite apparent that the USDA sire and cow evaluation program was in considerable need of additional fund support, Dr. Hodgson made extensive efforts to shore-up this important area of work. Fortunately, additional support was obtained in 1963 and as a result, the Dairy Branch of the Animal Husbandry Research Division was able to increase the effectiveness of sire and cow evaluation while initiating a modest research program.

Dr. Hodgson was the leader in the development of the Ad Hoc Committee several years ago which in turn was responsible for the development of the National DHIA Coordinating Group. This has resulted in a significant step forward in strengthening the administrative and organizational aspects of the National Cooperative Dairy Herd Improvement Program. It is with considerable pleasure that I present Dr. Hodgson to the Symposium and Workshop at this time.

DR. HODGSON: It is with pleasure that I welcome you to the Washington area on behalf of the Dairy Branch, the Animal Husbandry Research Division, ARS, and the Department of Agriculture. We hope that your two-day visit will be an enjobable and fruitful one.

As the Chairman indicated, it is true that I have had a great interest in this DHIA program and the related sire and cow evaluation activity through the years. I do not know of any program in the livestock industry in this country that is more dynamic, vital, and important.

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DAIRY DIVISION

by D. Chesley*

THE CHAIRMAN: It is with pleasure that I extend to you welcome to this Symposium and Workshop which we are dedicating the NATIONAL INSTITUTE FOR DAIRY RESEARCH AND WORKSHOP ON REPRODUCTIVE HEALTH OF DAIRY STOCK AND DOGS. The presence of each of you here this morning reflects your sensitivity to the importance of this Symposium to your lives, to contributions to our knowledge of this problem area.

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DR. BODGSON: It is with pleasure that I welcome you to the Beltsville area on behalf of the Dairy Branch, the Animal Husbandry Research Division, ARS, and the Department of Agriculture. We hope that your two-day visit will be an enjoyable and fruitful one.

As the Chairman indicated, as he said, that I have had a great interest in this DRIA program and the related uses and evaluation activity through the years. I do not know of any groups in the livestock industry in this country that is more dynamic, vital, and important.

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*Chief, Dairy Cattle Research Branch, ARS, U. S. Department of Agriculture, Beltsville, Maryland.

In many respects, dairy recordkeeping and mass selection has advanced much further than have related programs in other types of livestock. In poultry, the National Poultry Improvement Plan carries out a similar function. Their problems in operations are somewhat different and perhaps easier because breeding stocks are produced in many fewer units. Unfortunately, progress in performance testing and recordkeeping has not been great in other types of farm animals. I realize that your interest is primarily dairy. However, I feel that we need to be ever aware of needs and possible developments that may lead to extending these efforts to other species.

The National DHIA Program involves research, extension, education, and an increasing amount of administrative and organizational detail. You as researchers, are well aware of what is being done with the byproducts of this program. I feel that the research aspects of the program will play an increasingly important role in livestock improvement in the future. Large numbers of production records are available for analysis. From a cost of research standpoint, it is imperative that we maximize the use of these data. The extension, education, and operational aspects of the program are largely in the hands of dairy extension specialists. This we recognize as being desirable and is one of the reasons why this program has steadily grown in strength and effectiveness. It is therefore most important that researchers and extension workers coordinate their efforts to an even greater degree than the past. This is consistent with the view that dairy recordkeeping is one of the most important programs in dairy cattle improvement.

The National DHIA Coordinating Group was established to strengthen this vital recordkeeping program, with emphasis on its administrative and organizational aspects. It serves in an advisory capacity to the several segments of the industry who depend heavily upon the program. The Coordinating Group first met in February 1966 and again in May 1966. Already good progress has been made by this group. I feel that the Coordinating Group will from time to time call upon research workers for assistance in dealing with some of the many problems at hand. I am sure you will be responsive to their requests.

In conclusion, let me say that we appreciate your responding to our invitations to attend and participate in this Symposium and Workshop. I know that you have a full program and that you are eager to get it underway. I am sure you will have a very productive meeting.

THE CHAIRMAN: Thank you, Dr. Hodgson, for your timely comments and introduction to this Symposium and Workshop. They enable us to launch our program with a good start.

There have been many changes and improvements in the National Cooperative Dairy Herd Improvement Program, especially during the past 10-15 years. While the participation in the combined program is still only about 19% of all cows of milking age, this level of participation has been increasing through the years. Since 1954, participation in DHIA has doubled and currently approaches 3 million cows. Since 1955, production per cow in standard DHIA has increased nearly 2,500 lb. of milk. The production superiority of standard DHIA cows over all other cows not enrolled in recordkeeping has steadily increased and is now nearly 4,700 lb. of milk per cow per year. A major improvement since the early 1950's has been the development of processing centers that provide better on-the-farm recordkeeping services. Participation in central processing of DHIA records has increased to over 90% of all standard DHIA and DHIR herds. These technical services provide one of the very significant improvements in dairy recordkeeping. One of the byproducts of the DHIA program is the provision of production information for use by research and extension workers. The amount of these data being made available is increasing rapidly. The number of records made available for research and sire and cow evaluation has nearly tripled since 1954 and in 1965 numbered 1.75 million.

Another important step forward has resulted from the combined aspects of the multiple herd proof and the daughter herdmate comparison. The multiple herd proof has made it possible to more reliably estimate the breeding value of bulls. The daughter-herdmate comparisons provide us with a relatively simple, manageable, and effective method of indexing bulls.

Genetic progress for production traits in dairy cattle depends largely upon effective sampling and evaluation of the largest number of bulls possible as to their breeding value and in identifying and maximizing the ultimate use of those proven to be most superior. This is not to rule out the importance of evaluating cows and maximizing their use. In fact, we are extending considerable effort in this direction also. The major point being made is that the genetic appraisal of dairy sires and cows is a very important activity and merits the most critical attention possible. This is, after all, the reason for this Symposium and Workshop.

During the past few years we have taken a very large step forward in developing and using these tools for genetic appraisal of cows and sires. We know that greater genetic progress is being made today than was the case only a few years ago. It also seems possible that we may have reached a plateau in these developments from which vigorous and

well-aimed research will be needed in order to make further advances. Also, the need to recognize and define as clearly as possible existing and anticipated problem areas is more important today than in the past. This is particularly true for those of us who are engaged in estimating breeding values of cows and sires. The cost of computers, the cost of programming, and the lead-time needed to implement innovations are very important considerations. Also, let us remember the continuing need for objective and reliable determination of goals, urgencies, priorities, likelihood of success and cost-benefits. Support for research in the future will depend upon such criterions of justification.

Based on my own experience in recent years and based on communications with many of you, a need for this Symposium and Workshop was apparent. Credit for its planning and development should also go to Dr. Carter. The agenda that we have prepared reflects some of the more important problem areas about which we are concerned. Allow me to add to these the following questions which I hope your presentations, comments, and discussion will enlighten if you feel they are worthy of this purpose.

1. Are we effectively implementing the tools now available for maximizing genetic progress in dairy cattle production traits?

2. What step-wise or short-term improvements are needed for our existing methods of sire and cow evaluation? What are the priorities?

3. Are there better, different and more accurate methods available to us than the herdmate comparison? What are the operation problems? Are they feasible to use?

4. What, if anything, can be done to improve the non-AI or single herd proof?

5. What modifications or additions are needed to the input data being used in cow and sire evaluation today?

6. What operational improvements are needed? Are they feasible?

7. Have we reached a limit in scientific and technological improvements in our present methods?

8. What specific area of research is needed in sire and cow evaluation? What is the feasibility and likelihood of success in carrying out these studies? What are the priorities among them?

9. Where do we go from here in cow and sire evaluation--in supporting research projects--and in operational aspects of these activities?

In closing with these introductory comments I suggest that this be considered as a technical Symposium and Workshop involving basic and important problem areas and future research needs. In so doing, I urge each of you to probe deeply and interchange freely with no real concern as to operational details or as to policy and administrative involvement. You may also wish to limit discussion of the extension and educational aspects of sire and cow evaluation since this more directly concerns extension personnel.

I would like to encourage each of the participants to set your own pace, make your presentations as informally as you like, and allow discussions in a manner of your choice.

An Operational Procedure for the Use of In-Progress Records in Sire Evaluation

L. D. Van Vleck
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A desirable goal for sire evaluation is frequent evaluations using all information available at the time of evaluation. Since daily evaluations are not practical, evaluations every month, every two months or perhaps less often might be sufficient in most cases. Such evaluations should be made with all in-progress and completed records -- one test-day, two test-days, etc. These would include daughter records of the sires to be evaluated and the records of their herdmates.

The genetic implications of early evaluations are obvious. Such evaluations are probably almost as accurate as those based on complete records. The selection intensity will be the same either with in-progress or completed records. If so, the reduction in generation interval will lead to more rapid genetic progress which is inversely proportional to the decrease in generation interval. For example if enough first test day records are available to evaluate a sire, a decision on the sire may be made nearly a year sooner than possible with current methods. If decisions could be made on the average six months earlier with part records, genetic improvement would be 10% faster than with 305-day records only.

The real problems in early sire evaluation are operational -- the mechanical procedures needed to evaluate sires on all available in-progress and completed records. In order to apply any procedure certain parameters such as variance and covariance components and age factors will have to be estimated. This paper outlines one operational procedure which is analagous to methods now currently in use for completed records. The procedure also appears to be within the computational range of most computing installations. The parameters which research must find will be obvious but will be pointed out in the discussion.

The basic unit of data

The first step in the use of part records is to decide what the basic unit will be e.g., monthly test-day data or test-day data pro-rated according to number of days in the period. The primary use of part records will be sire evaluation. Therefore, the index equations will contain variances and covariances of all lengths of records used. The advantage of using monthly test-day records directly or standardized to a 30 or 30.5 day basis seems obvious.

There does appear to be some merit in adjusting these test-day records for the part of the test period when the test was made. For example, the record of a cow tested on the sixth day of her lactation and the record of a cow tested on the forty-first day are both regarded as first month records. Some adjustment would appear to be required for a at least the test day in the first month of lactation. Adjustments in later months may also be needed. This is clearly an area where some new research is required.

If only adjusted test day records are used, we will have the following kinds of records available for sire evaluation:

d_1, first test-day;

d_2, first + second test-day;

d_{10}, first + ... + tenth test-day. All are adjusted, if necessary, for the part of the test period when the test-day occurred. Note that only cumulative records are being considered.

Age correction for different lengths of lactation

The next step would be to correct these records for age at calving. Based on the work of the USDA group with 305-day records, separate regional factors will probably be needed. The work of Lamb and McGilliard in Michigan and Van Vleck and Henderson in New York indicates that different factors are needed for each length of part record, for season of freshening, and for milk and fat.

The easiest factors to find would be gross or ratio factors for joint age and season effects. This procedure was followed by Searle for New Zealand data and by Van Vleck and Henderson for New York records in their preliminary research. Averages are computed for each length of lactation group, for both milk and fat (a total 20 sets), and for each region in a fashion similar to that shown below for a specific age by season table.

Season	Age (mo.) ≤19	20	...	27	...	Mature	...	Old
1	$x_{1,19}$	$x_{1,20}$		$x_{1,27}$		$x_{1,mature}$		$x_{1,Old}$
2	$x_{2,19}$	...						...
3	$x_{3,19}$	...		"Base?"		"Base?"		...
4	$x_{4,19}$	...						...
5	$x_{5,19}$							
6	$x_{6,19}$	$x_{6,20}$		$x_{6,27}$		$x_{6,mature}$		$x_{6,Old}$

One cell is then chosen to serve as a base period. The gross factors are determined by dividing each entry in the table into the average for the base period. For example, the factor for age 20 months, in season 3 is

$$F_{3,20} = \frac{\text{Base}}{x_{3,20}} .$$

The next question is which cell should be used as a base. There would seem to be merit in choosing the base cell to be the cell corresponding to the average age of freshening for first lactations and the season of the largest number of freshenings since the primary use of part lactations will be initial sire evaluation. All records would be adjusted to a first lactation basis. Gravir and Hickman in Canada have discussed this possibility.

Note that there will be many sets of factors needed (no. of regions x ten for the different lengths of lactation x two for milk or fat). It might be possible to condense the tables, if necessary, by fitting some type of polynomial curve to the ratio factors.

All length of lactation records will be assumed to be age and season adjusted in the following discussion.

Herdmate adjustment

The next logical step is to adjust the records for the herdmate average. The methods of evaluation that Dr. Henderson will discuss are certainly as appropriate for part records as for 305-day lactations but for purposes of evaluation of contemporary sires the herdmate

method is much simpler although even it is not operationally simple.

The problem of adjustment for herdmate averages is the most difficult operational problem. Remember that we are using all records in progress and thus have records for one, two, ..., up to ten months of lactation. The problem of finding the appropriate herdmate average depends partly on the number of seasons we have. If we consider each calendar month as a season the problem is simpler than if we have longer seasons. For example, suppose a cow calves in calendar month three and she has records for five test-days. Her herdmates will be those cows which also calved in calendar month three. They also will have five test-days except for some which would have calved too late for the test day in that month. But, if we have seasons of four months then the herdmates of a cow will not all be in the same stage of lactation. The situation can be seen by using the following matrix.

Length of Lactation	Season of Freshening I				II				III			
	Calendar Month 1	2	3	4	5	6	7	8	9	10	11	12
1												
2												
3												
4												
5			*									
6												
7												
8												
9												
10												

*Suppose for example, a cow has completed five test-days of lactation after freshening in month 3 of season 1. She may have the following kinds of herdmates:

Herdmates

freshening in	have	length of lactation
month 1		5 + 2 = 7 test days
month 2		5 + 1 = 6 test days
month 3		5 + 0 = 5 test days
month 4		5 - 1 = 4 test days

In general if a cow has length of lactation, L, and freshens in month J(J=1,2,3, or 4) of the season, her herdmates will have lengths of lactation L+(J-I) for I=1,2,3,4.

The problem is to use the records of all herdmates regardless of their lengths of lactation to make the adjustment for herdmate average. If we are working with four-month seasons then there will be herdmates with four lengths of lactation. Suppose the averages for the four groups are H_1, H_2, H_3, and H_4 and the numbers of records in each average are n_1, n_2, n_3, n_4. The statistical problem is to find the best estimate of the true herdmate average, H_L, for a cow with length of lactation, L, given H_1, H_2, H_3, and H_4; i.e., we want $E(H_L / H_1, H_2, H_3, H_4)$ where E stands for the statistical expectation. The statistical basis is the same as that used for calculating the adjusted herdmate average as developed by Henderson, Carter, and Godfrey in 1954. A 1961 paper by Heidhues, Van Vleck, and Henderson describes the statistical details of that procedure.

The basic selection index procedure gives us $E(H_L / H_1, H_2, H_3, H_4) = c + b_1H_1 + b_2H_2 + b_3H_3 + b_4H_4$ where c is a constant and the b's are determined by solving the following set of equations:

$$\sigma_1^2 b_1 + \sigma_{12} b_2 + \sigma_{13} b_3 + \sigma_{14} b_4 = \sigma_{1L}$$

$$\sigma_{12} b_1 + \sigma_2^2 b_2 + \sigma_{23} b_3 + \sigma_{24} b_4 = \sigma_{2L}$$

$$\sigma_{13} b_1 + \sigma_{23} b_2 + \sigma_3^2 b_3 + \sigma_{34} b_4 = \sigma_{3L}$$

$$\sigma_{14} b_1 + \sigma_{24} b_2 + \sigma_{34} b_3 + \sigma_4^2 b_4 = \sigma_{4L} \qquad \text{where}$$

σ_i^2 = variance of H_i,

$\sigma_i^2 = \sigma_{h_i}^2 + \frac{\sigma_{e_i}^2}{n_i}$,

$\sigma_{h_i}^2$ = the herd-season component of variance for records of length i,

$\sigma_{e_i}^2$ = the error component of variance for records of length i,

σ_{ij} = the covariance between H_i and H_j (the herd-season component of covariance between records of lengths i and j from unrelated animals),

σ_{iL} = the covariance between H_i and the true herdmate average for records of length L (this is the herd-season component of variance if i = L and the component of covariance if i / L).

The analogy of this system to the one currently used for 305 day records may be useful in understanding the procedure. The equation to find the adjustment factor for the true 305-day (10 test-day) herdmate average is:

$$(\sigma_{h_{10}}^2 + \frac{\sigma_{e_{10}}^2}{n})\ b = \sigma_{h_{10}}^2 \ . \quad b = \frac{n}{n+\sigma_e^2/\sigma_h^2} \ . \quad \text{If } \sigma_e^2 / \sigma_h^2 = 1$$

this becomes the familiar n/(n+1).

As we can see the operational problems are rather large in this procedure. We must keep track of all herdmates of each cow by their lengths of lactation. Essentially this would mean, for any particular sire evaluation, separating the in-progress records into month of freshening groups since such groups would correspond to length of lactation groups. Then, depending on the seasonal groupings, herdmates for any particular cow would be from a subset of the month of freshening groups. This would be relatively easy to do if paternal half-sibs were not excluded. Excluding paternal half-sibs as herdmates would require storing the sire and production information for each cow in each freshening group.

In any case, the set of equations must be set up for each cow except that the equations for cows calving in the same month would be the same except for the n_i in the diagonal coefficients. Perhaps, the equations can be solved explicitly for each possible combination of stage of lactation and length of lactation.

Another situation which this method can handle is when the evaluation takes place before the end of the season. For example suppose that only two months of a season are included in the evaluation. Only two length of lactation groups would be available as herdmates. Only two equations would be set up. Similarly situations will arise at the end of lactations where only 8, 9, and 10 or 9 and 10 month herdmates would be available. Likewise, there will often be situations when one or more length of lactation groups will not have any records. For example, a herd may not have any cows freshening in June. Then for a cow calving in that season there will be no herdmates for the length of lactation group corresponding to June freshening. The equation corresponding to that length group would be eliminated from the set of equations. The number of equations to set up depends on the number of groups available.

The parameters needed for the herdmate adjustment are (1) the herd-season components of variance and covariance and error components of variance for the ten length of lactation groups, and (2) the breed-season averages for the length groups which are used in computing c.

Regression on herdmate average

The next adjustment needed is the within sire regression of daughter record on herdmate average. For 305-day records the regression coefficient has been about 0.9. If we ignore this step we will be assuming a regression of 1.0. These regressions should be estimated for each length of lactation.

Estimated Daughter Superiority

The last step is to combine the regressed and adjusted records of various lengths into an estimate of the sire's daughter superiority (EDS). This is a simple application of the selection index procedure although a rather large but "relatively small" matrix must be inverted to find the appropriate weights. The problem is this:

Find: EDS for 305-day production

Given: The averages of regressed and adjusted daughter records of up to 10 lengths, $\bar{d}_1$, $\bar{d}_2$, ..., $\bar{d}_{10}$.

The solution for all records expressed as deviations is the selection index:

$EDS = b_1\bar{d}_1 + b_2\bar{d}_2 + \ldots + b_{10}\bar{d}_{10}$ where the b's are the appropriate weights for the daughter averages.

The selection index equations for finding the b's are:

$$\sigma_1^2 \; b_1 + \sigma_{1,2}\, b_2 + \ldots + \sigma_{1,10}\, b_{10} = \sigma_{1,S}$$

$$\sigma_{1,2}\, b_1 + \sigma_2^2 \; b_2 + \ldots + \sigma_{2,10}\, b_{10} = \sigma_{2,S}$$

$$\sigma_{1,10} b_1 + \sigma_{2,10} b_2 + \ldots + \sigma_{10}^2 \; b_{10} = \sigma_{10,S}$$

σ_i^2 = the variance of the average of n_i daughter records of length i. Thus

$$\sigma_i^2 = \sigma_{s_i}^2 + \frac{\sigma_{e_i}^2}{n_i}, \text{ where}$$

$\sigma_{s_i}^2$ = the component of variance for sire groups for regressed, adjusted records of length i,

$\sigma_{e_i}^2$ = the error component of variance for regressed, adjusted records of length i.

σ_{ij} = the covariance between records of length i and length j of different daughters of the same sire. Thus

$\sigma_{ij} = \sigma_{s_i s_j}$, the sire component of covariance between records of lengths i and j.

σ_{iS} = the covariance between records of length i and the true daughter superiority, S, note that true daughter superiority is defined as one-half the additive genetic value of the sire for 305-day production. Thus

$\sigma_{iS} = \sigma_{s_i s_{10}}$, the sire component of covariance between records of length i and 10 month records.

These components of variance and covariance need to be estimated.

If later lactation records are used more equations can be added. If more than one record on the same cow is used the equations would have to be modified to account for the "repeatability" of records of various lengths on the same cow.

Decision for publication of in-progress evaluations

As a matter of review, the correlation between the true daughter superiority and the index estimate can be computed by the standard method as:

$$r_{TI} = \left(\frac{\sum b_i \, \sigma_{iS}}{\sigma^2_{s_{10}}} \right)^{\frac{1}{2}}$$

A decision to publish the EDS on in-progress records could be made on the basis of the size of the r_{TI}. For example an r_{TI} greater than that corresponding to twenty 305-day daughter records might be sufficient for publication. If desired, probability limits can be put on the EDS as: $EDS \pm z\,\sigma$ where z is the value taken from the table of the normal distribution coresponding to a selected probability of a greater value by chance and $\sigma^2 = (1-r^2_{TI})\,\sigma^2_{s_{10}}$.

Note again this entire procedure of using in-progress records is nearly the same as most current procedures. All I have done is extend the procedure proposed by Dr. Henderson over ten years ago to the case where more than one kind of record is used.

DISCUSSION

DR. BARR: I have a question here. I realize that this business of getting herdmates is a real problem and requires quite a bit of computing. Should we make any adjustment at all on the basis of a rolling herd average current to that particular part lactation?

DR. VAN VLECK: Do you mean a rolling herd average for complete records, or for in-progress records, or what?

DR. BARR: Well, the rolling herd average for the month of the records in question, that is being studied, whether it is complete or incomplete?

DR. VAN VLECK: Well, one couldn't do a very good job of adjusting for herdmate averages. My guess is that it probably wouldn't do nearly as good a job as using this procedure.

DR. BARR: I realize it wouldn't be as contemporary as this, because you have a full year.

DR. VAN VLECK: Actually, this procedure probably isn't too difficult, especially if the computer has any kind of speed and a good table look-up routine; if that is fast, then you can find the herdmates quite quickly. Your sire evaluation would be run from your herd file tapes rather than from particular sire file tapes, which means you would be running a larger volume of data through, and that is a problem. It wouldn't go through very fast for most computers.

DR. HICKMAN: One thing that bothers me is that there must be a relationship between a short record and a long record for different months of the year. That is, when both records start at the same time, the seasonal variation in yield of, say, 180-day records is quite different for the seasonal variation in yield for 305-day records, and for any particular month the relationship between 180-day and 305-day yield is quite different than it is for some other month. And I am wondering whether this can be taken into account in this particular procedure, whether these variances and covariances can be applied across months and across seasons or whether they would have to be evaluated each time.

DR. VAN VLECK: Right; what you are asking is whether there are several sets of equations or just one general set?

DR. HICKMAN: Yes.

DR. VAN VLECK: This may very well be, but my own opinion is that I doubt if the sizes of the variance and covariance will differ enough that we have to worry about it.

DR. FREEMAN: I think that we can add a little point here: Pete Spike just went through some 125,000 test day lactations on Holsteins, and the interaction of month and stage, if you express them as Chi Squares, was less than one percent of the total variance in all breeds.

DR. VAN VLECK: Did this include part records, as well as complete records?

DR. FREEMAN: Well, this was the test that they used in Ohio.

DR. VAN VLECK: Yes; along the same line, I think a bigger problem is whether you have herds at a higher level and herds at a lower level.

DR. FREEMAN: Yes.

DR. McDANIEL: Would you anticipate doing this in all?

DR. VAN VLECK: I think that the program would be more simple than you expect, but as far as the computer, it will not run very fast, or won't appear to run very fast.

DR. McDANIEL: I think the program is not so difficult to write but it will probably be very expensive to run.

DR. VAN VLECK: Well, that depends pretty much on the volume of input.

DR. FREEMAN: I would judge it would just be tracking data in.

DR. McDANIEL: We really don't have this much overlap now with our machines, and really, we are at the point that we can't load our computers with more data without seeing a pretty serious slowdown.

DR. VAN VLECK: I have no idea how fast this will go. We are nowhere near this stage in our work yet.

DR. TOUCHBERRY: All of the relationships on this are based on part records that were subsequently completed, is that correct?

DR. VAN VLECK: It couldn't be general here. But it may be necessary to modify that.

DR. TOUCHBERRY: Are there enough records that are completed, and is the difference here enough that, in other words, you may have part records included where the cow could have two or three months?

DR. VAN VLECK: This is a point that I think Dr. McGilliard will probably discuss in more detail. My thinking right now is that perhaps you should eliminate those kinds of erroneous records anyway, if they are erroneous, as far as the cow is concerned.

DR. TOUCHBERRY: They aren't erroneous as far as the bull is concerned.

DR. VAN VLECK: Maybe they are and maybe they are not; I don't know. We need a good criterion for deciding that, which I don't think we have now.

DR. BARR: Speaking from a strictly operational standpoint, it seems to me that just last year we eliminated one of the old problems -- this business of having incomplete records and erroneous records constitute all of the first proof on bulls -- what was the percentage in these early proofs?

DR. McDANIEL: We are running now about eleven or twelve percent incomplete.

DR. BARR: So, operationally, you might get into a situation where we are right back in that predicament.

DR. VAN VLECK: Yes, you need to decide where the record stops, because of a non-genetic reason or a genetic reason.

DR. BARR: Yes. But, you don't know; they all stop this month.

THE CHAIRMAN: Is there a measure -- and maybe you reported this and I missed it -- but is there a measure here that ties into or is used as a guide relative to the accuracy of this system, versus the 305-day system?

DR. VAN VLECK: Yes, a method we discussed right at the end of the presentation. You could use that or go to some back data and actually compare on a chart basis.

DR. HARVEY: As of a given time --

DR. VAN VLECK: Yes, as of a given time it would be at least as accurate. The efficiency of the data has to be at least as good or better.

THE CHAIRMAN: Because you have more data.

DR. VAN VLECK: Yes, because you have more data.

THE CHAIRMAN: And you would estimate that a generation interval would be reduced by how much?

DR. VAN VLECK: If you have enough information of first day records, you would save at least nine or ten months, but I could foresee lots of objections to that kind of procedure, and I don't know whether we have solid enough research to do that. Actually, I doubt that we do have solid enough research to say that we can evaluate genetic value for ten month production on the basis of the first test day average.

DR. LEGATES: So it would be a sequential proposition.

DR. VAN VLECK: If the bull were on a high enough basis he would be selected. If a bull were low enough on that one, he would never get high enough. It is the bulls in between that you have to delay the decision.

MR. RUMLER: The herdmates are not necessarily, are they, of the same length as the average of the information for the herdmates?

DR. VAN VLECK: Well, the herdmates will be enough, but they are really contemporary.

MR. RUMLER: Contemporary with essentially the same length?

DR. VAN VLECK: Right.

THE CHAIRMAN: Apart from this somewhat, would you care to comment on the feasibility or desirability of using some length of record other than the 305-day record, as a so-called standard for sire evaluation?

DR. VAN VLECK: Well, that is just an arbitrary decision which has to be made, and personally I would prefer a system such as we have here, because you are using all available information. If you are using, say, five month or four month or 180 day records, there are limits to their usefulness, but you are limited to 305 days now. But such use of fixed length records would of course be operationally much simpler.

DR. TOUCHBERRY: When you make your first run on the part record procedure, does a bull have to have a certain number of daughters with completed records?

DR. VAN VLECK: I would suggest that he doesn't have to have any.

DR. TOUCHBERRY: In other words, you would come up with a bull which has, say, twenty-five first test day lactations?

DR. VAN VLECK: Right. We could provide that information, and we could also provide the information that those are first test day records.

DR. TOUCHBERRY: O.K.

DR. VAN VLECK: People could make their own decisions based on what information was available.

DR. BARR: But you are still biasing it against the bull with the early proof though, versus the bulls that do have complete lactations. You have two groups, I think. You will be dividing the young sires from the bulls with complete lactations more than you are now.

DR. LEGATES: No, you are not; there are other aspects than just the one lactation involved. It is broader. In other words, do we take the 305-day lactation as the goal?

THE CHAIRMAN: I am a little concerned about this huge volume of data involved and the possibility of getting it, which, I realize, Dr. Van Vleck, you are not concerned.

DR. VAN VLECK: Oh, I am concerned with it, because we have already spent several months just getting our data ready to analyze.

DR. FREEMAN: There is one problem for which I see no good solution. And that is that you do need to treat terminal records, records that were terminated, in a different way. Suppose you do need to treat these separately from those that would go through a normal ten months; if we were using this procedure, you don't really know which they are at the time you are forced to make an evaluation.

DR. VAN VLECK: Well, perhaps you could delay the evaluation for one month and have that information.

DR. FREEMAN: If the one month lag time would be sufficient, you could do this, yes.

DR. VAN VLECK: If you could persuade your supervisors to report this information and to find this information, provided of course, that they know what information should be reported.

DR. McGILLIARD: I guess the other thing that bothers me a little bit is that in order to avoid becoming completely overwhelmed with the cumbersomeness of the procedure you are strapped with the monthly task, as we have it now, and you are sort of shoved away from forthcoming tasks and intermediate tasks.

DR. VAN VLECK: There is no reason why you couldn't use this procedure for random testing.

DR. McGILLIARD: Yes, but it really goes up geometrically.

DR. VAN VLECK: You are going to have to use some tricks anyway to reduce the number of combinations, but there won't be that many, although I haven't tried to do it, and so I might be completely wrong. If any system such as this were ever adopted, this would be on a supplementary basis for quite some time, I guess. It wouldn't be adopted overnight.

DR. BARR: Does this kind of system have the most merit for the needs of bull studs?

DR. VAN VLECK: Well, I think this might have more merit for them than anyone else. You are right, unless it were a routine enough thing to be useful to other interests.

DR. BARR: For herds that weren't on test.

DR. VAN VLECK: Yes, if you knew which herds were involved in testing.

DR. McDANIEL: There might be one other thing here to do with our seasonal calving patterns; it might be worth while to do this once a year, say, in March, on all of the cows that calved the previous fall. I am pretty sure that we wouldn't want to do this more than semi-annually because you distort your calving patterns when you are working on your two ends.

DR. VAN VLECK: Another point is that there won't be much advantage to using in-progress records unless you have a really large-scale bull sampling program. Otherwise, you won't find enough bulls through this procedure to be worthwhile.

DR. McGILLIARD: That's right.

THE CHAIRMAN: Any other comments or questions? Well, thank you very much, Dr. Van Vleck.

PROJECTION FACTORS FOR RECORDS IN PROGRESS AND TERMINAL INCOMPLETE RECORDS

L. D. McGilliard[a]

DR. MCGILLIARD: I have to admit that Dr. Van Vleck didn't say what I thought he would, or what I hoped he would, so I am going to have to adjust my discussion a little.

In any system of measuring performance of cows, I believe we sample and then try to establish the total performance from the sample. For example, for milk we have moved from a testing system where we measured all milk for a short time, 3 days, to complete measurement of milk for longer periods, 7 and 30 days. We have moved on to complete measurements for still longer, 305 and 365 days; and then we dropped back to sampling at periodic intervals and estimating totals for longer times from these samples--our present popular procedure of sampling one day per month and estimating total from these samples in various ways. We use a centering-day procedure, but there are other ways to employ these parts or samples to estimate what the total might have been. Too, we talk of even less frequent sampling and a whole variety of sampling variations, bimonthly, trimonthly, shotgun--where you send a tester twice a year or three times a year or whenever the dairyman isn't looking for him--and other variations. But all of these involve sampling and then trying to estimate the total from the samples.

In estimating total from the various samples, for the most part, we are attempting to put the animals, or the measurement of the animals' performance, on some equivalent basis so that we can make fair comparisons between the animals. Perhaps we don't have equal samples or fair samples, the same sort of samples, from each of the animals, so we extrapolate estimates to some total basis, so that they are comparable--hence, the use of projection factors for the various sampling periods to estimate total from the parts.

We can look at any of our testing systems and the way we estimate the total production for a lactation as the use of some sort of projection or weighting factors. With the centering day, we are giving certain weights to each test day. Now, we might give these various test days different weights from what we do in a centering-day procedure--and we could work out some weights which would estimate more accurately what the total for the lactation would be than does the centering date method--but with any of these procedures, projection factors come into play.

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[a]Michigan State University

We would like to compare the cows on some measure which we do not have for some cows but which we may be able to estimate from some partial measure that we do have for all cows. To project to a standard basis is one way to make fair comparisons.

An alternative to projecting to a total basis would be to limit our comparison to the least measure available for any particular cow. If we do this, we may ignore important information which would be quite useful and help us substantially in increasing the accuracy of our evaluation. We may even change the characteristics with which we are working. We may think that we are measuring the same characteristics, but the relationship may be such that we are actually redefining the trait in limiting our measure to something which is the least available for every cow.

Another alternative would be something like Dr. Van Vleck suggested, to take all possible combinations of performance available and to work with these as they are without projecting to a complete basis.

I think that is enough introduction to suggest where the projection factor becomes useful or might become useful. More will be considered a little later.

We might now suggest some of the situations in practice which we have for projecting milk production or components of milk to a complete basis. The first situation would be the record in progress, which Dale talked about. This is the record which is in progress at the time that the evaluation is to be made, and something needs to be done to use this record in the evaluation. A second situation would be records which are terminated short of completion. These are records that are terminated for some reason before they reach whatever particular point in time we choose to call a record complete. And a third situation in which projection factors might become useful would be where we have special combinations of parts. Rather than to accumulate monthly test days in sequence to a certain point and then to project, perhaps we might project certain parts which are more useful than others. Maybe we could use combinations like the first month, the fifth month, and the seventh month, or something similar. Or perhaps we might take only the fourth month. Or other special combinations of parts could be imagined.

Well, consider, first, records in progress and what uses we would have for projecting records in progress. These are fairly obvious I think, but I have jotted them down anyway. One is to make quick decisions in order to get rid of animals to make room for other animals to be tested--quick decisions, early decisions, the sort of thing that Dr. Van Vleck was talking about. Our second use for projecting and operating on these early parts of records in progress would be to shorten generation interval--again already suggested. Another opportunity for projecting would be where part of the record is environmentally

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controlled more strongly than other parts but genetically related to some other part which is less affected environmentally. In this instance we might want to exclude the part which is so strongly environmentally controlled and to emphasize the other part genetically related. The effects of pregnancy might be an example, where perhaps for a cow that conceives early, the latter part of the 305-day lactation may be affected rather strongly by pregnancy. You want to exclude the affected part, This would be an opportunity to project a record in progress to a complete basis excluding the part which was largely environmentally affected.

As for the records terminating short of completion--there would be two different categories of these to consider in projecting. One would be the first records of cows with no other information. The record is not continued until the cow is dry. It is terminated before completion. If you discard the partial record, you have completely lost information on the cow. Hence, this presents an opportunity to project to a complete basis and to try to use this information--if there is any information in this type of record.

The second sort of situation would be the later records on cows where a cow has completed one or more records, and then she has a terminal record which is not carried to completion. Now this might be a little different from the first record, because you do have previous knowledge of this type of cow. Maybe this terminal record will add some information if you wish to project it, or maybe it will confuse. But if some information is there, so is an opportunity to project, to salvage whatever information is available that might be related to the cow's ability.

The other situation for projecting is the special combinations of parts where we might find that some parts of the record are more valuable indicators of the cow's ability to produce in 305 days or for whatever measure you wish. Some parts might be more valuable, might contribute more information in evaluating the cow than other parts, and we could project and use these parts in proportion to their contribution to our knowledge. Examples of this type would be dropping terminal months, perhaps the last month or two months of a lactation which is terminated short of completion or even of a complete lactation. The information in later months might be nearly useless. We could discard these terminal months and have an opportunity to project the useful remainder to a complete basis.

A second opportunity with these special combinations of parts would be to lower testing costs and to get more cows tested by special types of tests where less sampling is needed--the shotgun test to increase the availability of tester resources.

Another opportunity with the special parts would be for herds just coming on test where, at the moment, we lose complete information for awhile. A herd begins to test, and we get no use of the records until perhaps a year later. By using projection factors to extend to completion, we could take the last 3 months of a lactation period or any other combination and estimate what the full lactation would have been.

Just for a moment let us consider the types of projection factors which have been proposed and are used--there may be some others a bit more valuable, but these are the common ones at the moment. The ones that have been used are some form of regression usually and have been of two main types. One is the ratio of the complete measure to the part measure--just a straight ratio of complete to part. This is in a sense a regression but a little different from a linear regression by least squares, the other type of projection factor which has been developed. Then there might be combinations of these using them both and in different ways.

In the way of a brief review of the differences between methods, the ratio, as you know, is a direct comparison of means, the mean of the complete measure to the mean of the part measure. The ratio in projecting ignores the incomplete repeatability of the various parts of the total measure. That is, if the various parts of the total measure are not completely repeatable,--if the correlation is not quite high--the ratio projection factor ignores this; and as a consequence then, in comparing the estimate with the actual, those that begin high, in general, will be overestimated, and those that begin low will be underestimated with the ratio projection factor because of the incomplete repeatability.

The ratio projection factor, however, does adjust the variation of the estimated to about the same variation of the completed records; so that when the estimated are mixed with the completed, the variation is somewhat similar where the ratio factor is used to project the part to the whole.

The linear regression factor--where fitted equations operate on deviations from means--in general, will estimate the completed record more accurately than will the ratio, particularly on the same data from which they are derived, of course. Although I have not seen any direct, good comparisons between estimates made from ratios and from regression factors on independent sets of data, I think that the difference would be so small that you would not be able to spot it. The difference is quite small even where the factors are applied back to the same data from which they were developed. I believe that in independent sets of data

the differences would be so small that you would not be able to detect them, but in theory the regression factors are more accurate if they are handled in the right way because they are developed from least squares.

The use of regression factors to estimate total yield will decrease the variation in the estimated amount, so that when those that are completed are mixed with those that are projected but incomplete, the projected records will be quite a bit less variable than the ones that were completed. This may create a small problem if these are not handled properly where both are used in the same system to evaluate sires.

The ratio, of course, will operate where you have a ratio of the mean of the completed to the mean of a part--usually only a single part--whereas with regression you can develop systems where various parts can be included and the estimate can be made simultaneously from several parts.

Just a word or two on the formation of the factors. This is an operational question of where to get these factors and what problems might be involved in the development of the factors.

There might be several ways to develop ratios of total to parts. One would be a ratio of the means where you have means over some groups of individuals for which you want to develop projection factors. You could average all of the completed records for a particular group and use this average as a ratio to the average of all of the parts. This is one procedure that could be used.

As an alternative, you might take for a particular cow the ratio of her complete record to its part, with a ratio for each cow then. The average of the ratios could be computed as a ratio factor for the group. There would be slight differences between these and the ratios of means. The ratios of the means, in general, would be smaller than the means of the ratios. This has to do, I think, with what variation is involved in the extreme cows and how they are included in obtaining the ratio. You see a little bit of this if you have looked at the projection factors which were developed in Michigan, the ratio factors which were developed in Iowa, and, consequently, the combination the two in the USDA factors. Our factors were means of ratios, the factors from Iowa were ratios of means, and the USDA factors were a combination of the two. They differ slightly because of this.

In forming ratio factors, there are two things operative which you need to watch--at least to be aware of--because they may change the factors sometimes in peculiar ways. One is the height of the lactation curve. Whether you are working with an average ratio or a ratio of an average of the total to an average of the parts, influencing this ratio will be the height of the lactation curve--the total amount of production. The other thing is the shape of the lactation curve. How high does it go at peak? How fast does it drop?

Both of these aspects in the development of the ratio factors become particularly important when we talk about terminal records because in the terminal records we have--or we may have--both a difference in the height of the curve where the culled cows are producing less than those that are retained. Now this decreased production automatically will change the ratio even if the curve of production through the lactation up to the time of termination were exactly parallel to the curve of the cows who complete the lactation. So just a change in the level if ratio factors are used will have something to do with them. Then also, in some types of terminal records the lactation curves are changed so that you have differences in both level and shape of curve.

In forming ratio factors, there may be some extraneous variables which have something to do both with the height of the curve and the shape of the curve. These need to be taken into account if you really want to put the cows on a comparable basis when you project from part to total and then intermix the extended records with complete records.

Of course, the breeds have differences in height and in shape of lactation curve. Consequently, most of the factors that have been developed have been within breed--for a particular breed.

Herds could well have something to do with production, and they do. But if you look at ratio factors from the whole population, probably the differences in the ratio factors for the different herds are so small that they are not worth worrying about. They can well be put aside from what has been seen so far. Likewise with the regression factors, the same sort of situation might be involved. I think Dr. Van Vleck says that even though with the regression factors you do need means to estimate totals from parts, these means for small groups may not be necessary, and you may do just about as well if you use means from large groups rather than small groups.

Ages of the cows at calving. Certainly there is some difference in both the height of the curve and the shape of the curve with changing age of the cow at calving. I suppose that you can break these ages into as many groups as you like. For practical purposes in most cases, these have been categorized into two or perhaps three groups--first lactations and later lactations for milk, and for fat, the differences are large enough that there may be three ages necessary. But depending upon the sophistication of your computing system and this sort of thing, you may want to have smaller groups of ages than that. The purpose is not to adjust for age the amount produced for the lactation. This has to do with the relation of whole to part record, and the adjustment is only to get close to estimating what the cow would have produced had she completed. Then the age correction for

the amount she would have produced as compared to a cow at base age, needs to be done on top of this. There may be a little interaction here that best could be taken care of in the way that Dr. Van Vleck has suggested rather than in, what seems to me, a more practical operational procedure of projecting to complete and then making the adjustment for age.

Season is another extraneous variable that has some effect upon the projection. Again, this doesn't adjust for the difference in level in seasons. It only takes care of a little bit of the level and the shape of the lactation curve which varies from season to season. The factors are smaller for cows calving through the season April through July in Michigan--the factors are smaller than they are for the rest of the year in the same age groups.

The different components of milk, if you have any interest in selecting for these and in evaluating animals for the components, are likely to differ among themselves and to differ from milk in the adjustments that will have to be made in projecting to a total. This is a problem at which only a brief look has been taken.

The other thing that I could say just a little about would be terminal records and what one might do in projecting these to salvage the information. I am not sure just how many of these lactations are lost before they are completed. (I think I am reasonably sure about this in Michigan, but everybody else tells me that I am not sure.) Reports go from six percent lost to eleven percent lost. Someone suggested eleven, I think, this morning. We measured upward of twenty percent lost in first lactation before they were completed, and I am not sure where the differences are. They may be in the length of records which are accepted, but I am not sure. If some people are accepting 180-day records and not worrying about less than 180, then maybe six percent or 10 percent. But if you worry about any cow that has even one test and is then lost--in Michigan either we are culling a lot harder or something else is strange. And as a consequence of our not using terminal incomplete records, these first lactations are lost for cows that might have been used as relatives to evaluate bulls. These records should be salvaged if there is any information in them, if there is any way to salvage them--and I guess this is not clear yet how much information is in the terminal records, even the first terminals. Whether discarding terminals has any bearing on estimating the breeding value of the bull is also not clear yet, and I would suggest it as one of the important questions.

At any rate, the terminal records, at least the first terminal records--if the tester or herd owner is at all careful in the recording of cows removed from the herd--can be divided into two groups. One contains those for which the herd owner had no say as to whether the cow stayed or not. She eliminated herself, and he had, for all practical purposes, nothing to say about whether she stayed or left. These records, in general, are quite different from the records where he did have a say about whether the cow stayed or left.

If there is some way that the disposals can be recorded correctly, to divide these into the two groups would be quite useful, and the types of projection and perhaps the usefulness of the record in evaluating bulls and cows would be quite different in the two groups. Our recording in Michigan is fairly inaccurate. Even with our own herds, I dispose of a cow for one reason, and the DHIA record comes back saying that she left for another reason.

In spite of this rough recording, if we group the records into those cases of cows that were disposed of involuntarily, where the herd owner really didn't have much to say about it so far as we can tell, these terminal records run nearly parallel in the shape of lactation curves to records of the cows which go on to completion. They are almost parallel. There is a little variation in them. They drop off just a tiny bit faster toward the last of the lactation period. They might drop more in the last month when something really went wrong, for example, a cow with severe mastitis when a herd owner had to get rid of her because she was so badly affected. But, in general, the involuntarily terminal lactations are just about parallel to the lactation curves of the normal cow and are at about the same level of production. They are slightly lower and they drop a little more, the shorter time the cow is in milk during that lactation, but they are almost as high. So we suggest, for the moment, if terminal lactations are to be used, to project with the normal factors for this group of cows removed involuntarily.

Now on the other hand, for those cows removed at the will of the herd owner--those that are culled--the records are quite different from normal in the level at the start of the lactation. The quicker the cow leaves the herd, the lower the curve. Cows that leave in one month are by far the lowest. Cows that leave in two months come next. So these records are distinctly different. If we are using ratio factors to extend these, right away this difference in level destroys the usefulness of the projection factors developed from complete records with ten test days.

[illegible] in Florida, at least the first terminal [illegible] data owner is at [illegible] carefully in the records [illegible] in the herd—can be [illegible] into two groups, [illegible] which the [illegible] owner had no say as to whether [illegible] were [illegible] Sis [illegible] heredity, and he was, for all [illegible] purposes, nothing to say about whether one stayed or left. [illegible] are quite different from the records where he did have a say about whether the cow stayed or left.

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The other thing is the shorter the record, the faster it drops off to the time that the record is terminated. Two-month records are not only lower in the first month but in the second month they drop way down. So they are not even parallel. As they lengthen, they are more nearly parallel, but they do drop off quite precipitously in the last of the lactation regardless of when the cow is removed. Where the cow is disposed of voluntarily, a separate set of projection factors is required to utilize these terminals by projecting to a complete lactation. And these factors are a little hard to form, you see, because you never had a complete lactation for them. You have the part but nothing beyond to which to relate it. The approach we have used so far to develop the ratio factors is to form ratios between adjacent months, and then from a series of ratios between adjacent months, we have been able to concoct a factor which combines all of these terminal voluntary disposals to get some factors which we guess might be somewhat useful to project what the cow would have done had the cow been able to complete. We may be overestimating even with these, but if we are, then some of these records are going to be so low that it would be rather useless to use the projection factor at all.

I don't know what to say about these terminals until I find out whether there is any information there at all. For the first calvers, there must be some information. How useful terminals are depends a little on the philosophy of what you are trying to evaluate in the cow--what the cow's real ability is. If you do as I do and say that the amount that the cow produces is an index of everything about the cow, and so anything that happens to her may well be related to her ability to produce--almost anything, I'll say--then you are going to use these terminal records in some way to evaluate the cow. On the other hand, if you say, "I only really want to know what the cow will produce under the best conditions," you may want to discard these or do something else with them. My own inclination is to use production as an index to evaluate the whole cow, the well being of the cow, everything about her, and in this sort of measure I am a little more interested than in the other types.

Now with the terminal records, how are you going to employ regression--other regression techniques--to develop projection factors with these incompleted terminals? I don't know. I am uncertain as to how this might be done.

I guess the other thing that I don't know that I want to know, is how do these various lactation curves differ in shape genetically: When we are tinkering with these records and projecting parts to total, is this entirely legitimate? I know something about the genetic relationship of the various parts of the curves. That is, I know something about the genetic relationship of the second month to the total, or of the second month to the sixth month. I don't know what the genetic relationship is in the actual shape of the curve. What sort of a number

do you put on the shape of a curve to measure this? If, in working in certain ways with these part records, we are altering genetically the shape of the curve, we may not want to do this. There may be some adjustment that we would want to do to include this as a separate characteristic. Maybe this relationship is not important, but breeders talk as if it is. They would like cows that produce the same amount throughout the lactation. No, they would still like to have the first part higher! But when the first is higher, they want the latter part brought up! Is there some genetic variation in the actual shape of the lactation curve among cows?

The other questions I have concern the practical use of incomplete records and some apply even to records in progress. I have suggested a question or so about the use of terminal records. What parts do you extend? Do you use individual months in some way? Do you use cumulatives? How early? Do you do different things with first records from what you do with later records?

With complete records even, are there certain parts that you would like to exclude before you use projection factors to estimate totals? Pregnancy would be one situation where you could cut out a section of the lactation. Conditions affecting the records--say a cow is recorded with mastitis on one particular test day. You could very well cut this out and use the rest of the months to estimate total. What parts do you want to use?

Terminal records--do you drop the last month and use what came before? Or do you drop off the last two? If the cow has a fourth or fifth month, do you just pick out that month? Those are really just about as good as the cumulative. What parts do you extend? This question needs answering.

I have just one comment about procedure in contrast, I think, to what Dr. Van Vleck is suggesting. My philosophy has been rather than to disrupt the routine for complete records, to extend to completion whatever part records we are going to use, in such a way that they can be included in the original routine for complete records without disturbance.

If one wants to use cumulative records to cut off everything no matter how short at the time of evaluation--even one test day record--extend and pump the estimates right in with all of the complete records, but weight them according to the amount of information which they contain. For example, if you have a cow with one test day, predict

what she would have produced had she completed. Then put that into the regular run with a weight which is appropriate to the amount of information which the record of that first month contains. It may be .6 in comparison with 1.0 for a complete record. This seems to me to be operationally a lot simpler than some other procedures. I think if you look at this early evaluation as really a rough screening--to put out the worst cows and to put a finger on the best ones--this may be as close as you really need to be.

DISCUSSION

DR. LEGATES: Well, this point of weighting these incompletes should also be used currently. I think this would help out our situation if we would weight these incompletes that we are now using, putting a proper perspective on these, rather than throwing them in as a total equal to the complete record.

DR. MCGILLIARD: Yes.

THE CHAIRMAN: It seems to me that this is a problem again that runs the gamut of the whole dairy recordkeeping program. I think that the Extension people here will acknowledge the fact that the CAR code is a difficult problem, and sometimes we are quite certain that the codes that we get are not nearly as representative or as characteristic of the conditions that have affected the record as we would like to have. And this, in turn, makes it difficult for us to even determine whether or not this is, in fact, a complete record or a short record that has been affected by certain conditions, or whether it is, in fact, a cow that is going dry or something as simple as this. This certainly involves our whole DHIA operation, and I think that this is an area that we need to be concerned with.

DR. MCDANIEL: For the records received during the previous six months, we have approximately one percent of all records with CAR codes indicating terminated by a dry date with less than 180 days in milk, and I don't think that we have that many cows milking this length; we have some one to two percent, and this is for Holstein records.

DR. MCGILLIARD: On what basis do you question not having that many?

DR. MCDANIEL: Well, are there that many cows that do not even milk 180 days?

DR. PLOWMAN: Yes.

DR. FREEMAN: May I ask a question here? Dr. McGilliard asked about whether or not there is information in these early records, and what information we could get. We recently looked at the percentage of bulls' daughters that were coded as having terminal records with the CAR sold for beef or died, and the correlation between this percentage of his daughters and the bull's estimated breeding value was .6. This tells me that the people who are milking the cows are selecting cows from the bulls which have higher estimated breeding values, this is indirect, but it certainly indicates farmers are selecting cows on their genetic ability.

DR. CARTER: I took a look at first lactations, and I have about 9.3 percent incomplete records during first lactation with a code of died or sold for beef and a 3.4 percent sold for dairy, which would make my total just under 13. But that is for Holsteins. But for my other breeds, this runs up between 18 and 20 percent. So there is quite a big difference in this for some reason or other.

DR. MCGILLIARD: Let's see, you have some that died too?

DR. CARTER: I included those with "sold for beef." I couldn't tell the difference. They had the same code in the record. But this was only on first lactation. I didn't put in the other lactations.

DR. VAN VLECK: I would like to formally withdraw that 6 percent figure that was used. This was on something that we did in 1960, and I think that the reason that figure was so low was incomplete reporting rather than incomplete records. And this month we are getting zero percent because our programer didn't have that information!

DR. MCDANIEL: Well, we know that in some cases here we actually are currently running thirty percent of the records reported incomplete, but a good portion of these are really complete, over the past years, it is closer to 14 percent.

DR. MCGILLIARD: I meant to mention this also if I didn't. This has a bearing, particularly, if you use ratio factors. The amount of culling has a bearing because if it is intense, it is going to change your records and your factors depending on how much culling is taking place.

DR. MEADOWS. Wouldn't you expect that records would be somewhat selective?

DR. MCGILLIARD: Yes.

DR. MEADOWS: Until your entire population was participating? I think that this would have something to do with the culling.

MR. RUMLER: Dr. Corley, how accurate do you think the DHIA CAR information really is? Fifty percent?

THE CHAIRMAN: I don't know. I am sure that it is not as accurate as we wish to have it.

DR. FREEMAN: An interesting comment here: If you include those cows that were coded either died or sold for beef and look at the production of all of those codes in the CAR records, including those that were affected by abortion, all of those were above the average. In other words, it is apparently beneficial for a cow to have been coded as having milk fever, mastitis, acetonemia--all of those sorts of things.

DR. STARKEY: Do you think it is true that these would have more difficulty?

DR. FREEMAN: I do.

DR. STARKEY: Rather than just an individual dairyman's idea?

THE CHAIRMAN: What should be the minimum length of record? What should be the qualifying point on the lower scale for length of record, before projecting--a one, two, three, or five-month basis? This could be subdivided into a terminal record category and a record in progress category.

DR. MCGILLIARD: My own opinion is this has to be anything I can get.

DR. PLOWMAN: Well, I think it is a matter of basic philosophy, as Dr. McGilliard has pointed out here, of what we want to evaluate; if this cow calves and she has twins and then a retained placenta, and she gets milk fever and ketosis and has breeding problems and so on, is this a genetic measure of the cow we want to estimate? Or do we just want to use the ones that go along and have no problems involved with their production? And if you want to take the first category, then, as Dr. McGilliard suggested, you have to take everything that you can get, but it may be that we should decide what we should do here.

DR. DICKINSON: Well, operationally, if you start making excuses for what you are going to throw out, it would be to some people's advantage to throw out a lot of the records. And I would say, operationally, I wouldn't make any exceptions. If you have information, use it, because if, in our sire summary, we say, "Exclude certain records", we will have a lot more inaccurate records than we see.

Could you then accept do you think the Data Gap by proceed?

[illegible] [illegible] [illegible] [

DR. PLOWMAN: I might ask a question of Mr. Rumler, in terms of all of the other breed organizations and yours, what length record do you accept for official recording?

MR. RUMLER: Ninety days, and some of the others will run up to 180 days. And, frankly, I agree with the Michigan philosophy over here, that perhaps the information that you get on incomplete records is more valuable to you than that you get on complete records.

DR. PLOWMAN: There can be a lot of culling in 180 days.

DR. MEADOWS: They are quite conscious as to when these records are. You bet your life, they are.

DR. PLOWMAN: The breeders are.

DR. MEADOWS: Both the entire herd and the breeders.

DR. TOUCHBERRY: Well, we should get some figure as to the number of daughters dropped. In other words, there may be some of this going on before that even.

DR. SMITH: There may be some criteria in herds that are using 100 percent AI.

THE CHAIRMAN: Does the group share the view that records in progress, or short records, that are projected and used in sire evaluation should be weighted according to some manner, according to the length of lactation?

DR. LEGATES: According to length of lactation.

DR. BARR: This is in addition to holding them until records with comparable calving dates have been completed.

DR. MCGILLIARD: These would be terminal records?

DR. CARTER: Would you use terminal records in a sire proof, if this were other than the first lactation, if you had a complete record of a cow?

DR. MCGILLIARD: Somebody else answer that. At the moment, I would say yes, but I really don't know.

THE CHAIRMAN: What are the experiences of others on this? I know you have some, don't you?

DR. CARTER: Well, I look around at these other fellows to answer. We do not use them now. If you follow through on this, even with these better cows, the terminal records tend to be below herd average. Dr. Van Vleck has put in a lot of work on this. And that raises the question that if something happens to that cow, are you more accurate in evaluating this bull if you exclude them than if you include them?

DR. MCGILLIARD: Well, you can twist this around quite a bit. My own philosophy is that a good cow is the one who can be hit and recover. That is the one I call a good cow. She runs along, something hits her, and she drops off; but she comes back up. A poor cow doesn't do that. What happens is that the good cow has three records; she comes back and makes the third record after a low second. Isn't this second record just like the terminal record on the poor cow except that this one we call good was able to recover?

DR. PLOWMAN: So you are asking to use this second one then?

DR. CARTER: The question is, what about the one that had something happen in the second? Does she remain in the herd?

DR. LEGATES: If you use them all, we are being more fair.

DR. MCDANIEL: I think that the thing that we need to know is on these one or two tapes that we have; it is presently below zero. I think that has more to do with it than that.

THE CHAIRMAN: I think Dr. Meadows' comment, too, in terms of not being selective in any way or encouraging any selectivity all the way along the line, but using all of the information, might be an argument for this.

MR. RUMLER: If you use any selection, you have to use a factor of the price of beef as well.

DR. CARTER: I have run off the comparison of herdmates in New York, looking at the records of potential dams and sires, and it is rare that one cow will not have a minus record as compared to herdmates. But something does happen to these cows, and some of them terminate with this happening, and some are kept around and recover, as Dr. McGilliard says. But I am not sure what the genetic implications are.

DR. MEADOWS: Well, I think this leads Dr. Freeman into his misinterpretation of Starkey's comment that the acetonemia cows are high producing cows because they don't give the poor cows a chance.

The poor cow gets acetonemia and we cull her, and I think this is what leads to it, and I doubt if that would lead to it if you were right.

DR. STARKEY: Well, I guess he was actually misquoting me.

DR. MEADOWS: Yes.

DR. LEGATES: Some of these things occur in an animal's life; is that his reasoning, that they have already gone through a culling for production?

DR. STARKEY: Yes.

DR. LEGATES: Which is also a contributing factor, I think.

DR. FREEMAN: Well, I think in some ways it is somewhat unrealistic to think of these CAR codes as ever being completely useful, because a cow is usually not sold for a single reason; it is a combination of things. She is a little slow breeding, and she is not really a good producing cow. So both things add together and she goes, where cows with only one problem may not.

DR. MEADOWS: Maybe we can teach our supervisors to code it voluntary, and then it can be broken down, but at least we could put it into the code as to whether it was voluntary culling or involuntary.

DR. MCGILLIARD: I think the original intent of CAR codes was to see whether some adjustment could be made in the records for the conditions. Apparently, we are not going to move very far in that direction because of incomplete coding, so maybe he is right to code whether I get rid of her or she gets rid of herself, which, I think, is the useful question for using part records.

THE CHAIRMAN: Are there any possibilities of making use of production on last test day as a means of classifying this record complete or incomplete, assuming that the information were at hand?

DR.MCGILLIARD: On last test day?

THE CHAIRMAN: In other words, if the cow is giving five pounds of milk, one might make the indication that she is dry or going dry, but if she is giving thirty pounds of milk on last test day, obviously this is an incomplete record. This thought has occurred to me from time to time, that perhaps this might be a scheme for better determining whether or not a record is completed.

Well, if there are no other questions on this topic, or comments, I want to again thank Dr. McGilliard for his very nice presentation on this subject.

ADJUSTMENT OF LACTATION RECORDS FOR AGE

B. T. McDaniel [a] and R. H. Miller

Whether we like it or not, it is usually necessary to adjust lactation records of dairy cows for age at calving for most uses. This is true even if the records are all of the same lactation number when there is any variation in the ages at which the cows calved. When records of all ages are combined and used, adjustments are clearly necessary. However, the less that records are adjusted, in terms of the differences between the actual age of the cows and the one to which the lactations are equalized, the less the likelihood of errors or inconsistencies.

BASE AGE

Equalization to some common base age is necessary when records of all ages are combined.

Mature equivalent. Traditionally, lactation records in the United States have been adjusted to a mature basis. However, the exact reason that adjustment to maturity was chosen is shrouded in history. This mature basis has normally been considered as the age of maximum production. The same general procedure is used in New Zealand, Norway, and parts of South America.

First lactation equivalent. On the other hand, the common practice in Europe is to adjust records to a first lactation basis. In several countries, only 2-year-old lactations are used, and they are not age-equalized. In Sweden and some of the other Northern European Countries, production records are corrected to a 2-year-old basis.

Mean or median age. An alternative procedure that would effectively remove variation due to age and have certain desirable statistical features would be to adjust to the average or median age. This would probably be about 4 or 5 years of age. An objection to this method is that the mean or median would probably vary more from sample to sample than age at maturity or age at first calving.

Percent of age class average. Another method, presently in use in Canada, is to express all records as a percentage of their age-class averages. The resulting values are free of age effects if the breed-class averages used are accurate.

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Constant weight basis. Some have suggested that records be adjusted to a constant body weight rather than a constant age. This has not been widely accepted for many reasons, one of which is that age is clearly an environmental result, whereas body weight possibly reflects both genetic and environmental effects. If weight were an entirely environmental consequence, there would be more justification for such adjustments. Clarke and Touchberry (1962) have discussed the problems involved in adjusting lactation records for weight.

Also, many studies [Clarke and Touchberry (1962), McDaniel (1964), Miller and McGilliard (1959), Syrstad (1965)] have shown that there is a significant effect of age independent of weight. In addition Syrstad (1965) has shown that first lactation cows yielded less than similar-aged second parity animals, although the first calvers were heavier. Third parity cows also produced more than similar-aged and heavier second calvers.

Another reason for using age rather than body weight is that age is easier to measure. The date the cow was born and the date she calved are all that is required to determine age; whereas weights depend on physical measurements. Weight estimates are also subject to measurement errors, depending on the condition of the cow at the time she was weighed and on day-to-day variation in stomach fill.

It appears that any adjustment for body weight or size should be in addition to, rather than in lieu of correction for age. Some additional accuracy might be gained by adjusting at least for within cow variation in weight.

In any event age partially corrects for weight differences.

Constant lactation number. Others have suggested considering lactation number rather than age. It has been shown by many authors [Gravir and Hickman (1966), Hillers and Freeman (1965), Miller (1964), Syrstad (1965)] that the regression of production on age within cows of the same lactation number is positive and important. Thus, adjusting only for lactation number does not remove all variation associated with age.

METHODS OF COMPUTING ADJUSTMENT FACTORS

There have been many procedures advanced for computing ratio factors or equations for adjustment of records to a constant age or to age of maturity.

Gross comparison. One of the most often used methods is the gross comparison attributed to Gowen (1920). The procedure is to simply obtain the average yield of cows at each age, and to form ratios between the mean

production at the age relative to which records are to be expressed (e.g., maturity) and averages for all other ages. Records are then multiplied by these ratios which should effectively remove age variation.

The main problem in gross comparison factors is that they represent not only the changes due to age and parity, but also the sum of those due to culling and genetic trend. In general, the difference in yield levels between different ages is due to an age effect, a parity effect, and a culling effect when genetic merit remains constant; otherwise, an additional genetic effect is present. Culling of older cows tends to bias factors derived by the gross comparison method upward for young cows. On the other hand, a positive genetic trend will make the young cows genetically superior, relative to older cows, and will cause a negative bias. Although in the past this genetic trend was considered negligible and of little importance, recent evidence [Burnside (1964), Van Vleck (1966)] suggests that it is about 100 lb of milk per year. This could lead to as much as a 500 lb difference between the genetic merit of young and mature cows, and would tend to have an opposing effect to selection in the biases on gross comparison factors.

Paired comparison. The paired comparison method, where comparisons are made between consecutive lactations of the same cow, was introduced by Sanders (1928). This method is normally biased negatively by culling, which is opposite to biases in the gross comparison method. However, probably the greatest problem with use of the paired comparison at the present time is the effect of and biases resulting from environmental trends. In the past 10 years changes in feeding of dairy cattle in the United States should have resulted in a constantly improving and more favorable environment (DHIA Newsletter, July 1965). Under circumstances such as these, the paired comparison factors represent the sum of the age effects and environmental trends. A study by Lund (1965) in a population where it was known that a major improvement had occurred in the environment verified that this type of bias is possible, since the paired comparison factors were larger than the gross comparison factors. In view of the consistent improvements in feeding that have occurred in the last decade, it is questionable if the paired comparison is of great value in estimating age curves for lactations made in the past few years.

Maximum likelihood. Miller et al. (1966) proposed that a maximum likelihood procedure, which would make use of within cow effects as in the paired comparison and between cow effects as in the gross comparison, be employed to estimate age curves. This method should at least theoretically be the most efficient method for estimating fixed age effects because it makes maximum use of both within and among cow differences. The investigators concluded that maximum-likelihood methods provide an unbiased estimate of the true age effects, independent of the effect of selection. Genetic trend, although not used in the statistical model, should have been partially

removed by other terms in the equation, such as year of calving. They concluded that maximum-likelihood factors should be used for applications requiring precise estimates of the true effects of age, free of any correlated effects.

The main problems in maximum-likelihood estimates of age are (1) the uncertain influence of errors in the parameters used in the equations and (2) the very large increase in computational labor involved (about 20-fold). At all ages the difference between the gross comparison and maximum-likelihood methods was lower than the variation between the paired and maximum-likelihood procedures. The gross comparison results were also closer to the maximum-likelihood curves than the average of the paired and gross.

Regression. Another procedure that has been used for developing age curves is the within-herd-year regression of production on age. Generally, when animals over the entire age span are used, it has been found necessary to use a cubic equation [Butcher (1966), Gravir and Hickman (1966), McDaniel (1964)]. The main problem with this approach is the stepwise increase in yield that occurs from one lactation to the next. Gravir and Hickman (1966) have shown that a regression curve fitted from all lactations will consistently overadjust the production of the younger 2- and 3-year-old cows and all 4- and 5-year-old cows, but will underadjust the production of late calving 2- and 3-year olds. This pattern was consistent for all four year-seasons studied. The same type of effect has been noted in large scale studies of DHIA records [Blanchard et al, (1966), McDaniel and Miller (1966), Syrstad (1965)]. It is likely that a much higher order polynomial equation (greater than a cubic) would fit the regression curve. However, considerable computational labors would be involved in fitting such a high order polynomial on a within-herd basis with large numbers of observations.

Ratio vs. additive factors. Additive correction factors have been developed from base age averages and used in New Zealand (Searle 1959). The additive correction has been shown to be influenced by the herd level [Searle (1959, 1960)]; whereas the ratio is relatively free of herd effects. Although this procedure is used in some parts of the world at present, there is no evidence that it is more accurate than the ratio method.

MILK AND FAT DIFFERENCES

Traditionally one set of age adjustment factors has been used to correct both milk and fat. Recent evidence [Butcher (1966), Gravir and Hickman (1966), McDaniel and Corley (1966), Miller et al., (1966), Plowman (1965), Syrstad (1965), Wilcox (1966)] has shown that age curves for milk and milk fat differ appreciably. The main difference between the curves is that young cows give a higher percentage of a mature yield in milk fat; and

older cows (6 years or more) tend to decline in milk fat yield faster than in milk production. Butcher (1966) reported that adjustment factors for fat percent varied from 0.96 for 2-year-olds up to 1.04 for old cows. Recent studies [McDaniel and Corley (1966), Plowman (1965), Wilcox (1966)] have indicated a difference of 0.02 to 0.04 between the factors for milk and milk fat yields of 2- and 3-year-old cows. Milk and milk fat ratios computed from the averages of 2-year-old production and peak yield given by Gravir and Hickman (1966) differ by 0.01 to 0.02. Syrstad (1965) found that fat percentage decreased about one-tenth of a percent between first lactation and maturity. An additional point is that some of these investigators [Gravir and Hickman (1966), McDaniel and Corley (1966), Wilcox (1966)] reported that the age of maximum milk fat yield occurred from 6 to 10 months earlier than the age of maximum milk production.

ENVIRONMENTAL INFLUENCES

Season of calving. Recent investigations by many authors [Gravir and Hickman (1966), Henderson (1965), McDaniel and Corley (1966), Miller et al. (1965), Simpson et al. (1966), Syrstad (1965)] have shown that age curves and the resulting ratio factors differ significantly for cows calving in different seasons of the year.

Generally the year has been divided into two seasons, winter and summer [Gravir and Hickman (1965), McDaniel and Corley (1966), Simpson et al., (1966), Syrstad (1965)]. However, Henderson (1965) stratified New York data into three seasons, and Miller et al. (1965) computed factors separately for four seasons. Under American conditions age correction factors for the summer are lower than those for the winter.

In one study [McDaniel and Corley (1966)] the lower ratios for the summer appeared to result from a differential effect of season of calving on age groups. The production of 2-year-old cows calving in the summer was only 2 to 3% below that of their contemporaries calving in the winter; whereas the production of older cows calving in the summer was 5 to 10% below that of their contemporaries calving in the winter.

Miller et al. (1965) divided years into four 3-month seasons, January-March, April-June, July-September, and October-December. The highest factors were for the April-June season, and the lowest for the July-September period. Factors for January-March and October-December were intermediate and similar to each other.

McDaniel and Corley (1966) computed factors after dividing the year into six 2-month seasons. They found that cows calving in March and April had the highest age ratios, while those calving in July and August had the lowest. Cows calving in and between November and February and in May and June resembled the March and April calvers, although they had slightly lower ratios. Cows calving in September and October had only slightly

higher ratios than those calving in July and August. These investigators concluded that two seasonal divisions would account for a large portion of the age by season variation. However, the year x season and 2-month-season x region interactions were not investigated.

Area and herd differences. There is substantial evidence that age correction factors differ among the geographical areas of the United States [Carter et al. (1963), Freeman (1965), Henderson (1965), McDaniel and Corley (1966), Miller (1964)]. It has also been reported that the percentage increase to maturity varies substantially among the geographical areas of New Zealand (N. Z. Sire Survey, May 1966). These differences may be reflections of the herd differences that have been found by some investigators [Hickman (1957, 1962), Hillers and Freeman (1965), Plowman (1965), Searle and Henderson (1959)]. Searle and Henderson (1959) found that for herds averaging 600 lb of milk fat, the multiplicative age correction factors were about 0.05 higher for 2-year-old cows than for 2-year-old cows in herds averaging only 300 lb butterfat (Table 1). The variation was about 0.04 for cows from 35 to 44 months of age, and about 0.01 for cows from 45 to 59 months of age (Table 1).

Age correction factors computed by the gross comparison method from tables of average milk and fat yields given by Syrstad (1965) for high and low herd levels were also consistently greater for the highest herd levels (Table 1).

Sets of factors developed from groups of high producing well-managed herds have been consistently higher than DHIA factors based on a large sample of herds [Lund (1965), McDaniel (1963), Plowman (1965)].

Hofmeyr (1956) studied the relation between herd level and the increase from first to second lactation in a small sample of Red Danish cows, and found some evidence that the relative increase was greater in higher yielding herds. In a group of 46,923 Swedish cattle, he found that the first lactation yield, relative to the overall contemporary herd average, decreased from 0.945 for low level herds to 0.858 for high level herds. Hofmeyr also found that the rate of increase in yield with advancing age among first lactation heifers was dependent on herd level. There was evidence that the increase was proportionally greater at higher herd levels.

Hillers and Freeman (1965) found that there were large differences between herds in the production increase with age among 2-year-old first lactation animals, but they did not relate this to herd level. Maximum likelihood age factors for herds at different yield levels will probably be necessary to completely resolve this question.

Time periods. The changes in age correction factors from one period of time to another are not well resolved. Carter (1966) has reported that there were only small differences in factors developed from New York data in 1963, as compared to an earlier set developed in 1953. Hillers and Freeman (1965) noted some small dissimilarities in age curves over a period of 13 years, but no consistent trends. Gravir and Hickman (1966) found that variation in slopes of yield-age curves between 2 consecutive years was significant, but was less important than seasonal deviations. Koh and Henderson (1962) found large age x year interactions, which also suggests that year diversities in age ratios might be important.

Differences among sires and cows. At least three studies [Barker and Robertson (1966), Hickman and Henderson (1955), Hillers and Freeman (1965)] have shown that there are genetic differences in rate of maturity within breeds, and it also is well known that breeds vary in this respect. In these studies rates of maturity differed between sires. Hillers and Freeman (1965) studied the effect of greater maturity on first lactation yield and the other investigators studied the change from first to second lactation. The importance of rate of maturity in itself depends on its correlations with first lactation yield and herd life, and how drastic the changes in the rate of maturity are among bulls.

The use of age correction factors that adjust to a mature basis does not change the selections that would be made among bulls with only first lactation daughters, as compared to those that would be made if only first lactation records standardized to a common age (e.g., 30 months) were used.

The problem of rate of maturity can be circumvented only by waiting until the daughters of bulls reach maturity before making decisions.

An important question is whether age correction factors should be developed for individual bulls when sufficient lactations are available.

Whether the increase in production with age is in similar proportion for high and low yielding cows individually, is subject to question. Although it would seem logical to expect low producers in first lactation to increase relatively more as they mature because of imperfect repeatability, the evidence is not clear. Johannson and Hansson (1940) interpreted some of their analyses to suggest that high producing cows increased their yields proportionally more with age than those with lower output. Barker and Robertson (1966) suggested that selection on high first lactation yield may also mean some selection for above average increase in yield to maturity.

Stage of lactation. Both Searle (1961) and Miller et al. (1965) have found that age correction factors for the first few months of lactation of young cows are higher than those for later months, reflecting the greater

persistency of younger cows. This decrease is rather drastic, and there are only very small age effects in individual monthly records by the seventh or eighth month of lactation. Age curves for cumulative lactations also decrease. McDaniel and Miller (1966) have found that the age correction factors computed from incomplete terminal records adjusted to a 305-day basis are slightly higher than factors based on complete lactations.

General. The foregoing review of results indicates that ratios among age groups are strikingly affected by various environmental circumstances. Factors such as season, region, and herd may be confounded with the progeny of individual bulls. In these cases, the failure to use sets of factors stratified for various environmental circumstances could lead to biases and inconsistencies in sire evaluations.

UNRESOLVED PROBLEMS

Although much is known, there are many outstanding and unresolved problems in age adjustment of dairy records.

Effect of errors in age adjustment on sire ranking. One of the more important problems is how errors in age adjustments affect sire rankings. It has been reported that there is a sizeable sire component for age [McDaniel (1964), Miller and McGilliard (1959)] and it has been the general feeling that errors and inconsistencies in age correction factors could lead to biases in sire evaluations. One problem centers on age effects among contemporary bulls, e.g., bulls of the same age used in the same herds, years, and seasons such as those in a progeny test program. It is likely that errors in age correction factors would be of relatively small consequence in these situations.

On the other hand, errors and inconsistencies among noncontemporary bulls that could have daughters in different herds, years, regions, seasons, or even at diverse ages, could be rather serious. Comparisons such as these are not normally made in a progeny testing program within a stud, but are made when younger sires are compared to previously proven bulls. When the sires of bulls to be progeny tested are chosen, such comparisons also are necessary. This could be especially important for large studs working in a nationwide area where the bulls are not represented equally in all regions and year-seasons.

The comparisons among bulls that were put in service at different times within the same stud are strongly influenced by age correction factors. Here, one bull is being contrasted on first lactation daughters to another bull that may have daughters that are 4 or 5 years old. If the age correction factors are too small, the proof of the younger bull will be biased downward, and vice versa.

Biological significance of difference. The biological significance and meaning of differences in age adjustment factors due to season, region, year, herd level, and their interactions, should receive study. Particularly, the effects of biological variation and the effects of differences occurring in ratios strictly from mathematical aspects should be investigated. Some questions might also be asked about feeding and management patterns between regions that cause differences in apparent rate of maturity. Why are older cows affected more strongly by seasonal differences than younger cows? Are carry-over effects of season of calving present in age factors?

Best method of developing factors. Another group of questions concerns the most satisfactory way of developing age adjustments. Should the factors used for age equalization adjust only for age and lactation number, or should they also compensate for the effects of selection? Should they be computed separately for different herd levels, or should they be developed for each individual herd? Should sets be developed for individual sires?

Best method of age adjusting. Another question centers around the best way of age adjusting. Is the multiplicative factor method now used the most appropriate, or should a regression equation be used? Another question is to which age should we adjust records? How much accuracy can be gained by equalizing to a 2-year-old basis compared to the current M. E. procedure? This is often mentioned but never studied. The question of what is the most important economic trait of a cow-lifetime production per day since birth, lifetime production per day since first calving, or lactation-yield in their first lactations may be relevant in this case.

TABLE 1

Age correction factors for different herd levels
(Adapted from Searle and Henderson, J. Dairy Sci. 42:833. 1959)

Age group range	Approximate percent of animals in group[a]	Multiplicative factors: Age corrected herd average low	high	Difference (high-low)	Average factor from NY data	Difference (high-NY)
(months)						
19-27	5	1.36	1.34	-.02	1.35	-.01
28-34	20	1.23	1.28	+.05	1.24	+.04
35-44	15	1.15	1.19	+.04	1.18	+.01
45-59	15	1.05	1.06	+.01	1.06	.00
Average[b]				+.02		+.01

Computed and adapted from Table 7, Syrstad, Acta. Agr. Scand. 15:46. 1965.

Age group	Multiplicative factor at different herd levels: low	medium	high	Differences: high vs low	high vs medium	medium vs low
1	1.303	1.291	1.299	-.004	+.008	-.012
2	1.166	1.182	1.190	+.024	+.008	+.016
3	1.135	1.133	1.144	+.009	+.011	-.002
4	1.052	1.071	1.072	+.020	+.001	+.019
Maximum yield (kg)	4,144	4,925	5,686			
Average[b]				+.012	+.007	+.005

[a]Taken from McDaniel et al. (1966)

[b]Unweighted

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DISCUSSION

THE CHAIRMAN: Are there any comments on this subject or questions for Dr. McDaniel? Age and adjustments for it have been a long-time problem.

DR. GAUNT: I hate to see age factors for individual sires, unless we had some indication of what the sire's proof would be without them; in other words what would individual factors do to the slow-maturing sire? It seems to me that this is something that a dairyman needs to know for a breeding program.

DR. McDANIEL: I was just mentioning this point. There are differences among bulls in age curves.

DR. HENDERSON: On a statistical matter, I would like to make it clear that the maximum likelihood model will not simultaneously estimate environmental trend and age factors; I will propose a way to do it tomorrow. Beardsley tried to estimate genetic and environmental trends amd age effects simultaneously. If you look at his results, he got sensible age factors and environmental trends, but nonsensical genetic trends. This is inevitable. You can't estimate these three simultaneously if you are controlling on the cow.

DR. McDANIEL: In our particular study, Miller actually didn't try to estimate genetic and environmental trends separately.

DR. HENDERSON: Fortunately!

DR. CARTER: I feel that these are things that we need to take a look at in our sire proving program, because as long as we use all ages for comparative purposes within herds, age factors can be a major source of error. Just from observation, one of the problems in the seasonal difference in the northeast is that the cows that calve in late winter and early summer are better cows that have had some breeding problems. Their calving intervals have slipped; they are very highly selected. I think that the results point this out. If we are going to compare those with these two-year olds, then perhaps we should adjust for this selection.

DR. McDANIEL: This is where I think philosophy enters. Should age factors adjust for selection as well as age? Or, should we adjust strictly for age? We did not notice differences in percentages of cows in the various age groups from season to season. We do notice, however, that we don't have many senior two-year olds in the winter season, only a lot of junior two-year olds.

THE CHAIRMAN: Would anybody take a stab at reflecting on the relative accuracies of multiplicative, regression, and maximum likelihood factors?

DR. McGILLIARD: I would say that there isn't any good way to compare them, because they do different things, and you can do them in one step or separate steps.

DR. HENDERSON: You can do M.L. on the logarithm of the record, and then you can do different things.

DR. TOUCHBERRY: I suppose it depends, really, on what you are trying to do with the age factors, doesn't it? What is the measure of what you are trying to do?

MR. RUMLER: Down to two-year olds.

DR. HENDERSON: Well, I guess many others, too, have stated--- that the purpose is to estimate what the cow would have produced had she been mature, rather than the age she actually was when she made the record. Whether or not this is a proper goal, I don't know, but this is what some people have stated.

THE CHARIMAN: Are there any other comments or questions?

DR. FREEMAN: Just one: Dr. McDaniel alluded to it, but if you look at test data, there is a big age by stage of lactation interaction, and it is just another way to say that the lactation curves are quite different by ages of cows.

CONSIDERATION OF MATES OF SIRES

George R. Barr[a]

First of all, on behalf of Dr. Starkey and myself, I would like to express our appreciation to you for the opportunity of being able to participate in this workshop. I think that it is an excellent idea, and I hope to see many more of them in all fields of animal production.

Of course, one of the recurring questions in sire evaluation is the relative importance of the selection of the mates of the sire in affecting that sire's proof.

Now this question, of course, is most often raised for bulls whose daughters are milked in a small number of herds or one herd. However, with differential pricing of semen, and concentration of advertising, this particular question is being raised more and more for bulls which are being used in AI situations. Today I propose to raise some points for discussion, and these are as follows:

(1) Herdmate comparisons are effective in reducing environmental correlations among paternal half sisters; (2) An AI proof with records expressed as deviations from herdmates constitutes the most accurate method of sire evaluation currently available.

The next five points I consider to be questions for which there seem to be no clear-cut answers at present. I plan to spend more time on these points later, and by that time I hope that you will have done some more thinking about these and will contribute materially to the discussion.

In terms of background, in 1965 research was begun in Wisconsin in cooperation with the Holstein Friesian association, under the project title, "Evaluation of Sires Used in Selected Herds" -- and I would like to emphasize that word "Selected" - "The Evaluation of Sires Used in Selected Herds". One of the objectives of the study was to use existing techniques to develop more suitable methods of evaluating sires used in small numbers of herds. A combination of information on daughters, dams, and their herdmates was one of the methods proposed. The data consisted of 160,00 plus records made by about 68,000 cows in 450 herds throughout the United States. To further illustrate the uniqueness of these data, the period of time involved was from July of 1953 to March of 1961. During that period of time there were over 9,900 sires

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[a]University of Wisconsin, Madison.

used in those 450 herds--this amounts to about two new sires per herd per year. Of these sires, there were about 1,900 that had ten or more daughters, and about 1,300 that had ten or more daughter-dam pairs. Herdmate comparisons were computed for all records, using current USDA procedures, including a rolling seasonal average.

Now I would like to present some of the results of this work to you,and I thought that the best way to do it would be to present the results within the framework of the paper written by Dr. Lush in 1944. The philosophy of this paper is outlined briefly in the Appendix. Now those of you who are familiar with this paper, of course, recognize the formula at the top of the first page of the Appendix where Dr. Lush has stated that most sire indexes could be written in the form: $I = a + c(X - bY)$ where I is the index or measure used for comparing one bull with another; a, of course, is a constant which brings the average of the whole group of indexes to some desired level; c is a constant which can be used to expand or contract the variability of I; X is the average of the daughters' records, Y is the average of the dams' records; and b is a constant which determines the relative emphasis on Y as compared with X.

Now if you think of this formula in terms of herdmate comparisons, c would take on the well-known value $N/(N + 20)$, and b would take on the value 1. So this is how a herdmate comparison could be expressed, using this same index. I have rewritten one here in the more conventional form:

$$I = b_1 X + b_2 Y$$

where b_1 in equation 1 is c and b_2 is $-bc$.

Now, of course, we want to maximize the correlation between this index and the bull's true breeding value. This is r_{IG} and the values of the b's which will accomplish this for us are given there in the center of the page. Dr. Lush has indicated that the correlation between the average of the daughter and the average of the group of dams to which that bull is bred can be written according to the formula on the second page of the Appendix.

I have also included a copy of the path coefficient diagram from the paper. The diagram describes the causes of the correlation between X and Y. Remember that X is the average of a group of daughters and Y is the average of their dams. We have correlations among daughters of

a sire; this is w in the diagram. We have correlations between the daughter and her dam, which is r in the diagram. We have correlations between a daughter and the mates of a sire other than her own dam, and then, of course, we have the possibility of correlations among the dams, themselves, to which this sire is bred. These are v and u, respectively, in the diagram.

An analysis was made of these production records that I have described to obtain estimates of these correlations, and these estimates were obtained or were calculated from records both unadjusted and adjusted for herdmate production. The estimates obtained for the correlations are given in Table 1.

Remember that the value for r represents the correlation between a daughter and her dam, and v represents the correlation between the record of a daughter and the record of a mate of her sire other than her own dam. We normally assume this to be zero; the two calculated values are given in columns 2 and 3 of this table. The path u is the correlation between dams bred to the same bull, and once again we usually assume this to be zero. W is the paternal half sib correlation and, of course, we normally assume this to be $h^2/4$; the values obtained are given in the table. r_{GX} is the correlation between the bull's breeding value and the average of his daughters, as outlined, making the normal assumption that the paternal half sib correlation is strictly $\frac{h^2}{4}$.

The correlation between the bull's breeding value and the average of the dams is assumed to be zero.

If you look at the results in the center column of Table 1, you will see that the correlation between the daughters and dams other than their own is higher than the correlation between dams and their own daughters. This says that the dams of daughters other than the daughter in question are more highly correlated with the dam's own daughters. This correlation, of course, could be biased upwards if the dams make their records in different herds. Remember that in the center column, the records are not adjusted for herd differences. My opinion is that this is the reason for the high correlation.

In the right hand column, the most apparent feature is that the values for v and u are, in fact, very close to zero. Once again, I think this demonstrates that herdmate comparisons are highly effective in removing environmental correlations among paternal half sibs.

Using the estimates from Table I, I have computed values for b and c and also the expected improvement in accuracy by including the dams versus leaving them out. This is the column headed $\frac{r_{IG}}{r_{GX}}$ and it increases with increasing numbers of daughter-dam pairs. This is no doubt due to the correlations that exist, the value of u and v that were estimated.

Turning to Table IV, one rather surprising thing there is that the amount of emphasis you place on the dam now carries a plus sign instead of a minus sign after you get beyond the ten-daughter level. Probably more important is the ratio of the correlations on the right-hand side, so that for all levels or all numbers of daughters and dams, the increase in efficiency is very small.

Are proofs made in one herd worth considering? Would we perhaps be better off to simply ignore this single herd information, and make one selection strictly on the basis of pedigrees? Before we can even consider this question, we have to decide for whom are we selecting these bulls. I think that if we are picking them for AI situations, obviously, we have a time factor involved. Just from a strictly generation standpoint, we are better off to pick the bulls on pedigrees, because we know they are going to be around longer, because by the time a bull has a proof in one herd, and then you have to wait again to get some information from AI, he is just a bad risk. Also, we have to weight the kind of selection differential we can get from pedigrees versus the kind of selection differential we can get when we examine bulls on one-herd proofs.

It seems to me that if we wanted to really test this for an AI situation, this could be done by simply taking bulls' pedigrees and their one-herd proofs, and comparing these to their AI proofs. Of course, to make this accurate, you would have to take into account when the information becomes available. You wouldn't want to use all of the information on a bull's pedigree. You would want to use the amount of information that was there when the bull was born, or you would run into similar situations for picking them as for a single-herd proof. So I would like to ask several questions of the group here:

First should we even consider, for any use at all, proofs made in one herd?

Question number two:

Should sire proofs made in one herd ever be listed with proofs made in many herds?

I, personally, feel that for the foreseeable future, this isn't really too feasible, and I would certainly welcome right now any opinions on this matter.

DR. HENDERSON: Well, perhaps I had better wait until tomorrow before doing that. Whether or not it should be done is not the question, but I will have a procedure for this if it isn't a case of preferential treatment of N. S. daughters. I am not asking you whether we should do it. It can be done, I believe -- with that one assumption, no preferential treatment.

DR. BARR: That is a pretty big assumption!

DR. HENDERSON: Probably too big.

DR. BARR: Question number three:

The fact remains that breed associations in particular have had the daughter-dam comparison as their official sire proving system, and we all say that environmental manipulations can be made to make the proofs look good or bad. The question was raised that, if we, as a group, go to herdmate comparisons, environmental manipulations are, in fact, easier with daughter-herdmate comparisons than they are with daughter-dam comparisons. I hadn't really thought about this before, and it is something that certainly is open to question.

Question number four:

Will the use of daughter-dam comparisons expressed as deviations from herdmates improve the accuracy and/or reduce the biases in proofs made in single herds? When we talk about accuracy now, we can consider the accuracy for a single bull or the accuracy of genetic selection in the population. Certainly, in a DHIA population, there would be substantial loss in accuracy simply because a large number of cows don't have their dams recorded. For the data that we studied, this was not a problem. About ninety-five per cent of the daughters had dams with records.

So, once again, these data are a somewhat unique, so that I think that inferences from these data to a DHIA population are really not feasible. However, in a DHIA program, you would lose a large number of cows, simply because they don't have any dam information.

Question number five:

How do environmental correlations among daughters and dams affect the relative emphasis to place on daughters and dams in sire proofs?

I hesitate to make any definite conclusions based on the results that we got. But I do think that before we even seriously consider a daughter-dam comparison situation, where records are expressed as deviations from herdmates, that we would have to investigate further the kinds of correlations and determine whether or not they are even worth taking into account, or whether we would be better off simply to take the values as they are found in Table II, assuming that the environmental correlations are zero.

I would welcome any discussion on this topic.

DISCUSSION

DR. HARVEY: This study that you made did not take into account differential matings of cows with different kinds of sires?

DR. BARR: No.

DR. HARVEY: So that the dams would really have a bias and little differences, genetically, between them. How important do you think that this really might be? In that case, wouldn't this use of dam information be far more important than what you have indicated?

DR. BARR: Yes, I calculated some values with genetic differences among the dam groups, and they change the values around pretty drastically.

DR. LEGATES: We do have some information on this same point, using a sub-sample of these bulls that George was talking about. About 600 of them had nine or more first lactation daughters.

In one case, computing the breeding value just on daughter deviation and the second case just on daughter deviation plus the dam deviation, the rank correlation was about .97 between each group, and in addition, there were about 99 of these bulls that had AI proofs of twenty-five or more daughters, and relating the AI proofs to the daughter deviation as contrasted to daughter deviation related to dam deviation, why, we had

less than one per cent increase in precision by using the complete index.

DR. BARR: I guess that we are really conservative at heart, as animal breeders. But I have read over several papers, including one that hasn't yet been published, and most of them are fairly critical of the idea of even worrying about the dams. This is true in Dr. Lush's paper, before we were even seriously considering herdmates. But they always end up with the qualification, "This might be important in certain single conditions in terms of a bias, especially for single herd proofs." I know that several of you people in this room have made that same qualification.

DR. MEADOWS: And the cause of that is, this really refers to the intra-herd differential needs, didn't it?

DR. McGILLIARD: Yes, that's right, differential herd information.

DR. MEADOWS: With respect to genetic level.

DR. McGILLIARD: Yes, this would be in respect to the AI population.

DR. MILLER: The average bias would be about 40 pounds of milk per sire, according to some of our results.

DR. FREEMAN: Well, we did this a little bit different way in the cows. One of them was just straight Iowa DHIA data, and the other was California ABS Data. We took all records of deviations from herdmates, and then took the dams that the bulls were mated to, and did a between and within sire analysis, so that if the bulls were mated preferentially, there should be an average difference between the dam's production over various sire groups. These all were non-significant.

DR. BARR: Just the value u from the diagram, as you can see.

DR. FREEMAN: Yes.

DR. HARVEY: Well, for those in AI, in fact isn't this becoming a more important problem all the time?

DR. FREEMAN: Yes.

DR. HARVEY: Isn't it because of the value of semen?

DR. BARR: Differential pricing of seman.

DR. HARVEY: Because breeders are beginning to use specific sires more for specific cows.

MR. BALDWIN: Yes, they are using high producing sires for all the cows, overwhelmingly on the high producing cows on the high-level sires. Apparently we are going to be in an interesting situation where the bulls are going to be proved at random, and then be put in a pricing system where, eventually, they will be herdmates.

DR. RUMLER: Is it a fact, or isn't it, Dr. Barr, that all of the data that we have used, and all of the information that we have, is based on the assumption that there is no economic selection pressure at all, no economic pressure in any of this data, and when you apply those economic pressures, you may have a different situation then than when you have data that has no pressure against this, and is this a factor of practical human nature, versus straight analysis of data?

DR. BARR: I don't know. But this brings up a question that I would like to ask: Are the conditions of sire proving, specifically with respect to breed associations, uniquely different enough from DHIA, the kind of situation where we seem to be geared to -- are they different enough from each other to warrant special methods for proving sires for breed associations for their sire recognition programs?

We had a graduate student calculate sire-son correlations based on USDA sire evaluations. He had one hundred-and-some-odd sires that were used in AI, and about 250 of their sons. The average deviation of these 100 sires, of the 250 sons, was plus 17 pounds of milk. The sire-son correlation was .46. The average deviation of the sons was about -14 pounds of milk. Now this indicates we are not making a great deal of genetic progress. I am not saying that these absolute values are really measuring the breeding value of the bulls, but I do think that they indicate that the group that were picked to be sires were not substantially better than breed average for production.

DR. LEGATES: There is a genetic trend in there through the sire to the son.

DR. BARR: Well, allowing for genetic trend, what per cent of the difference is this going to represent?

DR. LEGATES: It depends on what the slope is.

DR. BARR: This is over a time period from --

DR. LEGATES: Five years, probably.

DR. BARR: Yes.

DR. LEGATES: Get Dr. Carter to repeat what he told us at lunch.

DR. CARTER: Oh, yes, this is about where everyone goes through this period, and I guess this is where we were twenty years ago, and I hope we are ahead of it now.

DR. BARR: I am not really accusing AI of this. We are not doing what we should be doing, though.

DR. LEGATES: There is a point, though, before you leave that these bulls may not have been used proportionately.

DR. BARR: Oh, yes, they were weighted.

DR. LEGATES: You weighted them?

DR. BARR: Yes. Well, the results, I think, that Dr. McDaniel had and Dr. Freeman gave are not weighted. The weighted results were .42 for milk and .46 for fat, but they essentially remained the same.

APPENDIX

Lush (1944) stated that most sire indexes could be written in the form:

$$I = a + c\ (X - bY) \qquad (1)$$

where:

I = the index or measure used for comparing one sire with another.

a = a constant which brings the average of the whole group of indexes to some desired level.

c = a constant which can be used to expand or contract the variability of I.

X = the average of the daughters' records.

Y = the average of the dams' records.

b = a constant which determines the relative emphasis on Y as compared with X.

Equation (1) can be rewritten in the more conventional form for a selection index:

$$I = b_1X + b_2Y \qquad (2)$$

where: $b_1 = c$ and $b_2 = -bc$ from Equation (1)

We want to obtain solutions for the b which will maximize r_{IG}, the correlations between the index and the sire's true breeding value. These solutions of course are:

$$b_1 = \frac{r_{GX} - r_{GY}r_{XY}}{1 - r^2_{XY}} \cdot \frac{\sigma_G}{\sigma_X}$$

$$b_2 = \frac{r_{GY} - r_{GX}r_{XY}}{1 - r^2_{XY}} \cdot \frac{\sigma_G}{\sigma_Y}$$

Lush (1944) has illustrated that r_{XY} can be written:

$$r_{XY} = \frac{r + (n - 1)v}{\sqrt{1 + (n - 1)u}\ \sqrt{1 + (n - 1)w}}$$

where:

r = the correlation between the record of a daughter and the record of her own dam.

v = the correlation between the record of a daughter and the record of a mate of her sire other than her own dam.

u = the correlation between the records of two mates of the same sire.

w = the correlation between the records of two daughters of the same sire.

Analysis was made of Holstein production records to obtain estimates of r, v, u, w and h^2. These estimates were calculated from records both unadjusted and adjusted for herdmate production. Results are in Table I.

TABLE I: Values for r, v, u, w, r_{GX} and r_{GY}

	Normally Assumed	Estimated from Records Unadjusted for Herdmates	Estimated from Records Adjusted for Herdmates
r	$.5h^2$	.207	.151
v	0	.296	-.017
u	0	.336	.035
w	$.25h^2$	.383	.133
r_{GX}	$\sqrt{\frac{.25h^2}{1 + (n - 1)\ .25h^2}}$	*	*
r_{GY}	0	**	**

* Computed from the formula $\sqrt{\frac{.25nh^2}{1 + (n - 1)w}}$ with h^2 = .25 based on results obtained from additional data.

** Assumed to be 0.

TABLE II: Values for b and c when $r = .5h^2$, $v = 0$, $u = 0$, $w = .25h^2$, $h^2 = .25$, $r_{GX} = \sqrt{\frac{.25nh^2}{1 + (n - 1)\ .25h^2}}$, $r_{GY} = 0$ with varying numbers of daughters

Number of Daughters	c	b	$\frac{r_{IG}}{r_{GX}}$
1	.127	.125	1.01
5	.506	.125	1.01
10	.808	.125	1.01
20	1.151	.125	1.00
30	1.341	.125	1.00
40	1.461	.125	1.00
50	1.544	.125	1.00
100	1.743	.125	1.00
500	1.943	.125	1.00
1000	1.971	.125	1.00
10000	1.997	.125	1.00

TABLE III: Values for b and c when r = .207, v = .296, u = .336, w = .383, $h^2 = .25$, $r_{GX} = \sqrt{\frac{.25nh^2}{1 + (n - 1)w}}$, $r_{GY} = 0$ with varying numbers of daughters

Number of daughters	c	b	$\frac{r_{IG}}{r_{GX}}$
1	.131	.207	1.02
5	.367	.594	1.22
10	.522	.714	1.36
20	.683	.790	1.50
30	.766	.819	1.57
40	.817	.834	1.61
50	.852	.843	1.64
100	.931	.862	1.70
500	1.007	.878	1.76
1000	1.018	.880	1.77
10000	1.028	.882	1.77

TABLE IV

Values for b and c when r = .151, v =-.017, u = .035, w = .133, h^2 = .25, $r_{GX} = \sqrt{\frac{.25nh^2}{1 + (n - 1)w}}$, r_{GY} = 0 with varying numbers of daughters

Number of daughters	c	b	$\frac{r_{IG}}{r_{GX}}$
1	.128	+.151	1.01
5	.410	+.072	1.00
10	.569	-.002	1.00
20	.713	-.105	1.00
30	.783	-.172	1.01
40	.824	-.219	1.01
50	.852	-.255	1.01
100	.918	-.348	1.02
500	.985	-.458	1.03
1000	.995	-.475	1.03
10000	1.004	-.491	1.03

REFERENCE

Lush, Jay L. The optimum emphasis on dams' records when proving dairy sires. J. Dairy Sci., 27: 937-951. 1944.

PREFERENTIAL TREATMENT

H. W. Carter[a]

DR. CARTER: As I look over the program, I find myself the only Extension man and since we in Extension are mostly responsible for raising questions, not answering them, that is mainly what this paper will do.

Some of you may be familiar with a paper that was presented in 1961 at the American Society of Animal Production, in which Dale VanVleck and a group at New York looked at the selection of dams for some sires that were used by farmers who purchased semen from other farmers. I will present the results on selection of the dams here, just to give you what we found at that time.

Table 1. Deviation of Daughters and Dams from Herdmates

Sire	No. Dtrs.	Daughter Average	Dau. Deviation from Herdmates	Dams Average	Dams Deviation from Herdmates
A	91	13,125	- 277	13,911	- 285
B	43	16,154	+ 2863	14,430	+ 599
C	44	14,075	+ 650	13,986	+ 334

These were bulls that had been used fairly heavily by New York dairymen, and you will see that Table 1 gives you the results for these sires. I have labeled these "A", "B", and "C". The first one had 91 daughters, the next 43, and the next 44. In the middle column the deviation from herdmates of these daughters is a minus 277 for sire "A", a plus 2863 for sire "B" and a plus 650 for sire "C".

It is interesting to note that sire "A" was used on below average dams. When we compared those dams with their herdmates, the deviation was minus 285 pounds of milk. This is a sire that was sold basically on type, and I think that they were looking more for show type, animals that they might show, rather than for production, but I am guessing slightly on this.

The next two sires were production sires and you will notice that there was fairly high selection on the part of the dams for both "B" and "C".

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[a]Animal Science Extension, Cornell University.

Table 2. Deviation of Herdmates from Breed Average

Sire	Daughters Herdmate Production	Breed Average	Deviation from Breed Average
A	13,296	12,277	+ 1,019
B	13,333 lb. milk	12,277	+ 1,056
C	13,386	12,277	+ 1,109

All of these sires were later used randomly in A.I. This is why we selected them for this study. Notice, however, in Table 2 the high selection on the part of dairymen who used these sires. The average dairymen, and by this I mean average DHIA dairymen, didn't use these sires. There is more selection among dairymen in their choice of bulls than there is among dams within these herds.

I have used a heritability of .25 and assumed that if we adjust for the selection on the part of the dams, we would adjust the daughters' deviation from herdmates by one-eighth of the dams' deviation. To adjust for herd selection we would use ten percent, or one-tenth. I have taken this a step further and have adjusted these for the number of daughters by the regression of N over N plus 15.

Table 3. Adjustments for Dam and Herd Selection and Number of Daughters

Sire	No. Dtrs.	Adjustment when dams are included: Superiority Over Herdmate	Dam Adj.	Herd Adj.	$\sqrt{\text{Dtrs.}}$ Adj.	Adjusted Daughter Difference
A	38	- 203	+ 36	+ 168	.72	- 0
B	33	+ 2660	- 75	+ 114	.69	+ 1862
C	44	+ 632	- 42	+ 110	.74	+ 518
		Adjustments Ignoring Dams				
A	91	- 277		+ 102	.86	- 151
B	43	+ 2863		+ 101	.74	+ 2193
C	55	+ 650		+ 115	.79	+ 604

Table 3 shows that the adjustment for the selection of dams in the case of sire "A" is a plus 36 pounds of milk, for "B" a minus 75, and for "C" a minus 42. Since only a part of these daughters had records on their dams, the regression is much lower on the top part of this table than in the lower part, where we ignore dams. When we adjust for herd effects and for numbers, we end up with a prediction of future daughters of sire "A" of zero deviation, sire "B" of a plus 1862 pounds of milk, and sire "C" of a plus 518. At the bottom of Table 3, where we ignore the selection among the dams, you will notice that our prediction is higher on two sires and lower for one by using the additional daughter records and ignoring the selection among the dams.

Table 4. Herd and Number, Daughters Adjustment and Decrease by Year to the Last Summary

	1961 A.I. Sire Summary		Last Sire Summary		Difference Between	Yearly
Sire	No. Dtrs.	± Dev.	No. Dtrs.	± Dev.	Two Proofs	Change
A	91	- 155	213	- 367	212	106
B	43	+ 2193	573	+ 1338	855	214
C	55	+ 604	1154	+ 182	422	106

All of these sires were used randomly in A.I. at a later date. In one case we had an A.I. proof three years later, and in the other case, five years later. Unfortunately, I didn't have the information on this for the other sire. You will notice there that the thing we need to look at is yearly change. The yearly change for sire "A" was 106 pounds decrease. The yearly change for sire "B" was 214 pounds, and for sire "C" it was 106.

Now let's say we look at only two-year-old records in New York State, and that we have a sire who had a proof in 1961, of plus 100. In 1962 we look at only those two year olds freshening one year later compared to herdmates; instead of plus 100, he would be only 48--we would be dropping about 52 pounds a year. Our normal drop should be thirteen pounds a year, if we keep adding an equal number of two year olds to a sire's overall group, and what we find here is that these three bulls averaged 116 pounds.

I use this as a means of pointing out that even though we adjust for the selection among the mates of these bulls, there is something else that we do not adjust for that has a sizeable influence on the results.

All that we can point to is the fact that when dairymen went to a special effort to arrange semen and then to arrange someone to breed the cows, for which they also had to make special arrangements, they not only did not breed their average or their poorer cows to these bulls, but apparently they gave a little special care to the daughters after they were born. I am not saying that this was it. It would appear that this is what took place. I would call this a non-measurable influence with which we are confronted.

To measure this another way, I looked at some bulls that New York used for special mating to get sons; these are bulls that had done a really good job in the A.I. stud where they were originally used. NYABC purchased some sons of these bulls, trying to do better than the Wisconsin study George Barr showed for young sires. The result was that dairymen in New York said, "if NYABC thinks enough of these bulls to buy their semen for sons we think we will use them."

As a result of these matings, we have a sizeable number of heifer calves of these bulls in New York. The production figures in Table 5 show what happened.

Table 5. New York versus USDA Proofs on Selected Sires

Sire	New York Results		USDA Summary		Superiority in N.Y.
	No. Dtrs.	Milk Dev.	No. Dtrs.	Milk Dev.	
Burkgov	211	+ 1,636	1,768	+ 960	676 # Milk
Oliver	58	+ 653	3,679	+ 180	473 "
Ivanhoe	1,206	+ 657	8,978	+ 457	200 "

On the left, you will see the number of daughters in New York and their superiority after we have made adjustments for herd effects and for number of daughters.

In the next two columns, on the right, is the number of daughters on the USDA report which would include, on "Burkgov" for example, the 211 daughters in New York.

Notice that we have an inflation here of 676 pounds of milk for "Burkgov"; for "Oliver" we have a plus 473 pounds of milk; and for "Ivanhoe" on a very large sample, we have a plus 200 pounds of milk.

There are differences in age factors that can account for some of this difference. But I think that these go quite a bit beyond what you would expect to account for with age factors. This is another indication that when people think they have something special that they tend to give it a little special care, which has an influence on the evaluation of the sire, and complicates the problem of ranking sires.

I would like to read the last paragraph that I have here, so that I will say what I intend to.

"These data would question if the premium price sires handled by some A.I. studs might not have inflated proofs also."

Some of these studs that do handle a special sire at an extremely high price, I am sure, may have the same type of situation that I have just been reviewing.

"Since the amount of this inflation cannot be measured, then perhaps these sires should be labeled with a special identification. Would these inflation factors be the same as those for non-A.I. sires used in several herds"?

I don't know whether they are or not. I am raising questions.

"Where do these unknown factors fit into our national sire evaluation program"? These answers are needed if we are to use sires evaluated under these conditions in our efforts to make maximum progress in improving the genetic merit of our dairy cows for milk production.

DISCUSSION

DR. BARR: Could I just quote this environmental project? I realize that there are some believers and some non-belivers in this kind of thing in this room. I guess that I was, at one time, listed as one of the non-believers. But using this environmental evaluation program, we have been able to measure rather substantial differences among herds, and I wonder if there is some merit in at least looking into this a little further for evaluation of preferential treatment within herds? Now this isn't something that can be done in a computing center; you have to go out and talk to farmers and try to devise ways of measuring this.

THE CHAIRMAN: George, would you amplify that a little bit more, and give a little bit of the background as to what this is all about for those who are not as familiar with it?

DR. BARR: You have been associated with it a lot longer than I have. This is a long-time project that has been going on in cooperation with the Animal Husbandry Research Division, of course, and it tries to account for differences in herds as they are affected by differences in management of these herds.

And those of you who were at Dairy Science heard an example where we had a chap go out and evaluate a hundred herds, and they were actually

given environmental scores to see if he could evaluate the management of the cows and the level of feeding.

As for level of feeding -- that is one thing in which maybe we are ahead in Wisconsin--these cows were all getting enough feed, and this didn't make any difference. So, using this approach, and visiting these herds once--since the repeatabilities were reasonably high--we were able to account for a fairly substantial proportion of the differences among herds in the production level.

And I have often wondered if we maybe shouln't try to push this idea a little further. I think that we have run into a dead end so far as trying to do this statistically is concerned--preferential treatment; maybe you don't agree with me, but I certainly don't see any way of handling it.

DR. HENDERSON: George, the man who did the evaluation of these herds--

DR. BARR: Yes?

DR. HENDERSON: What did he know about the production levels of these herds?

DR. BARR: Nothing. He got it from data after he visited the herds.

DR. HENDERSON: He had no way of knowing?

DR. BARR: Well, of course, if the dairyman is really interested in his cows, he starts showing his herd average; but this fellow was good enough that he was very objective.

DR. MCDANIEL: I don't know; this is just my personal opinion. I don't work with cattle out in the field. But it only takes about one pound per day over the lactation of a two-year old to give what I was talking about here, once they rate correctly; if they get one extra pound from each cow or each two-year old each day for the lactation, they have received five or six hundred pounds. But what happens if you walk in this herd and look at these cows, and this fellow points out one particular heifer first? I think that when he walks into the barn, that is the heifer that he looks at first, and when he goes to the feed rack and gets feed, he picks out the best bale, and I don't think that all of this really is intentional.

DR. BARR: That's right.

DR. PLOWMAN: Oh, it is intentional, all right! It is human nature!

DR. MCDANIEL: And I wonder--I wonder, really, if we can pick it up by looking at our DHIA grain feeding--I thing we might.

DR. BARR: He won't even record that. No, I mean just go and ask the man.

DR. MCDANIEL: But a case like this now, where you have a lot of daughters, I wonder if it might not just show up there.

DR. BARR: Sure.

DR. FREEMAN: The other problem is, at least in the Midwest, where grain is not expensive, there are a terrific number of cows that just eat all the grain they can while they are in the parlor, and if that isn't enough, they get some from the silage in the bunk outside.

THE CHAIRMAN: Do you feel, George, that you could detect this kind of thing by herd visitation of the type that you might do through environmental studies, or environmental data recording?

DR. BARR: I don't really know.

THE CHAIRMAN: This might be difficult, mightn't it?

DR. BARR: But I think that somebody ought to try it.

DR. GAUNT: You mean pick out the preferential treatment to individual cows within a herd?

DR. BARR: Well, the two are confounded; the two are confounded, yes.

DR. TOUCHBERRY: Are all herds the same?

DR. BARR: No, we have just estimated this kind of thing for a thousand cows in about thirty herds, and much to my surprise it is negative.

DR. MCGILLIARD: Well, may I suggest that maybe all of this preferential treatment isn't bad, and that maybe we are actually getting a positive correlation between different types of environment here, and making it more accurate?

DR. BARR: It must be!

DR. MEADOWS: Well, really, you are talking about two things: In one, you are talking about the use of high-priced bulls. And the other, you are talking about the preferential treatment of daughters.

-I wonder, really, if we can pick it [illegible] rain wading [illegible] we might.

BARR: He would even [illegible] I mean just go and ask the [illegible]

DR. MCDANIEL: But a case like this now, where you have a lot of daughters, I [illegible] it might not just auto[illegible] are.

BARR: Sure.

DR. FRIEDMAN: The other problem is, at least in the Midwest, where grain is not expensive, there are a terrific number of cows that just eat all the grain they can while they are in the parlor, and it isn't enough, they [illegible] from the village in the bunk [illegible]

THE CHAIRMAN: Do you feel, George, that you could detect this kind of thing by herd visitation of the type that you might do through environmental [illegible] or any [illegible] data recording? [illegible]

DR. [illegible] don't really know.

THE CHAIRMAN: This might be [illegible] migrant's life?

DR. BARR: But I think that somebody ought to try.

DR. GAUDY: You mean pick out the preferential treatment to individual cows within a herd?

BARR: Well, the two are confounded; the two are confounded, yes.

DR. FOUCHERAY: Are all herds the same?

DR. BARR: No, we have just estimated this kind of thing for a thousand cows in about thirty herds, and [illegible] to my surprise it is negative.

DR. MCGILLIARD: Well, may I suggest that maybe all of this preferential treatment isn't bad, and that maybe we are actually getting a positive correlation between different types of environment here, and making it more accurate?

[illegible] you are talking about two things. The [illegible] use of high-priced bulls. Are the other [illegible] differentials [illegible] of [illegible] there.

DR. BARR: But the two are confounded.

DR. MEADOWS: They are for awhile.

DR. MCGILLIARD: For awhile, yes.

DR. MEADOWS: I would guess that the thing that has led to the most error in the single herd proofs when we have purchased bulls for AI, that for no known reason the bulls that we actually buy just happened to be born at a fortunate time. I guess I have bought more AI bulls than anybody in this room, and I am pretty sure that the fortunate bulls that get purchased are those whose mates, for some reason, did not have a good chance, and without any effort on the owner's part, the daughters came along when everything was real good; the AI manager has no choice but to buy these bulls because he has got to have some to breed, so those are the bulls that we use. But most of the young bulls sampled are sampled on heifers, and again you have little choice when you are just breeding to a bunch of heifers later on.

DR. BARR: Well, one of the problems in picking is that you really haven't looked at the problem as to the maximum, you know. You just don't get the information.

DR. MEADOWS: And if Chuck will listen, I guess in AI we are really looking at the daughters of the bulls that have been selected by the AI units. We don't know how we could have improved on their accuracy in choosing. In general, it has been very poor, as is pointed out from the results, and there may be a more accurate way of choosing.

THE CHAIRMAN: One of the questions that you raised George, I believe, is should the single herd proof be listed along with the results of the multiple herd proofs. Now I didn't quite get what you meant.

DR. BARR: I didn't mean for the same bull. I didn't mean a one herd proof and an AI proof on the same bull. To me, they are two groups. And should we put them together or not? And I guess we can.

DR. HENDERSON: We can!

DR. BARR: Whether we should or not is another question. We can, statistically.

DR. BARR: But the two are confounded.

DR. MEADOWS: They are for sunlike.

DR. [illegible] Yes.

DR. MEADOWS: I would guess that the thing that has led to the most error in the single herd proofs when we have purchased bulls for AI, that for no known reason the bulls that we actually buy just happened to be born at a fortunate time. I guess I [illegible] more AI bulls [illegible] time room, and I pretty sure that the fortunate bulls [illegible] purchased are those which, for some reason, did not have a good chance, and without any effort on the owner's part the daughters came along when everything was real good; the AI [illegible] has no choice but to buy these bulls because he has got to have some breed, so those the bulls that [illegible] use. But most of the young bulls sampled [illegible] sampled [illegible] uniform, again you have little choice when you [illegible] sending to a bunch of heifers later on.

DR. [illegible] Well, one of the problems in [illegible] is that you really never [illegible] the problem as to the maximum, you know. You just [illegible] get the information.

[illegible] And if Chuck will listen, I guess [illegible] we are [illegible] of the bulls that have been selected by the AI units. We [illegible] how we could have improved on their accuracy in choosing. [illegible] general, it has been very poor, as is pointed out from the results, and [illegible] be a more accurate way of choosing.

[illegible] CHAIRMAN: One of the questions [illegible] you raised because, I [illegible] should the single herd proof be listen along with the [illegible] of the multiple herd proofs. Now I didn't quite get what you meant.

DR. BARR: I didn't mean [illegible] the same bull. I didn't mean a one herd proof and an AI proof on the same bull. To me, they are two groups. And should we put them together or not. And I guess we can.

DR. HENDERSON: We can.

DR. BARR: Whether we should or not is another question. We can statistically.

DR. CARTER: I have been raising that question for quite a while. I feel that maybe we encourage equal weighting in the two groups because of the way that we are listing them, and maybe we should take our listing and let one section of the listing be AI proofs, and then the other non-AI's, and then I raise the question as to some of these so-called AI's, as to whether this description really fits them or not.

DR. FREEMAN: When we mail a list of sires to Iowa dairymen, and we do--on sires available to Iowa dairymen, we list two groups--AI proven and non-AI.

DR. GAUNT: USDA puts them out together. But we do it, too; AI goes out as one group.

DR. LEGATES: You do have a point on the listing. Someone said that it was easier to give preferential treatment to the herdmate daughters than it was to the dams--I am not sure that has been discussed now.

DR. BARR: I am not saying this. I have heard this expressed by other people. But it is pretty obvious.

DR. HENDERSON: You can't do anything about what has already happened.

DR. LEGATES: The other thing that I raise in rebuttal, and that is you are allergic to this, but whereas the other is history, you can never uncover it, just what is there. So there are points in both directions.

DR. BARR: Well, how do you evaluate it when you do see it?

DR. LEGATES: Well, either way, and that is the other thing that I would say about preferential treatment was what to look for. And you see, I go out and say, "Well, he knows this bull's daughters, and knows this other bull's daughters, and knows these", but unless I have some criteria to examine and look for, I am still just looking.

DR. MEADOWS: Well, if you ever give--I think Dr. Lush made this statement maybe thirty years ago--if you ever give preferential treatment to one group of cows, you won't ever sell another bull. If I give preferential treatment to cows, and if I compare daughters and dams, I have had it!

MR. ARTHUR: I have been raising that question for quite a while. I feel that maybe we encourage equal weighting in the two groups because of the way that [illegible] are listing them, and maybe we should take our listing and let [illegible] for [illegible] the listing of groups, and [illegible] Non-AI's, and [illegible] related questions as [illegible] of these [illegible], whether [illegible] weekly [illegible]

DR. [illegible] Dutch [illegible] of [illegible] to Iowa dairymen, and we do--on minds available [illegible] training; we list two groups--AI proven and non-[illegible].

DR. [illegible] Usen puts them [illegible] together. But we do it, [illegible] AI goes [illegible] one group.

DR. LEGATES: You [illegible] a point on the listing. Someone said that it was easier to give preferential treatment to the herdmate daughters than it was to the dams--I am not sure that has been discussed now.

DR. BARR: I do not doubt this. I have heard this expressed by other people. But it is pretty obvious.

DR. HENDERSON: You can't [illegible] anything about what has already happened.

DR. LEGATES: The other thing [illegible] I raise in rebuttal, and that is you are allergic to this, but wherever the other is history, you can never recover it, just what is there. So there are points in both directions.

DR. BARR: [illegible] evaluate [illegible] when you do see it.

MR. LEGATES: Well, either way, and that is the other thing that I would say about [illegible] the [illegible] look for. And you see, I go out and say, "Well, so knows this bull's daughters, and knows this other [illegible] and [illegible], but unless I have some criteria to [illegible] look for, I am at [illegible] looking.

M. MINADOWS: Well, [illegible] ever give--I think Dr. [illegible] made this statement [illegible] thirty years ago--if you ever give preferential treatment to one group of cows, you won't ever sell another bull. If I give preferential [illegible] to cows, and if I con[illegible] re daughters

DR. CASON: Just buy different kinds!

DR. BARR: Well, just by accident!

DR. MEADOWS: Well, but if you preferentially treat a cow and then use her as a dam, I think it builds up in her record.

DR. TOUCHBERRY: It is not so much what you can do about it. I think that the record is there, and you can certainly bias a contemporary comparison more than you can a daughter-dam, because you have got all of the cows there at one time.

DE. GAUNT: Yes, there are both ways on this, depending on the market.

DR. HENDERSON: The pressure now is actually to make a cow look good. But there is no incentive to make a bull look good, though.

DR. MCGILLIARD: In discussing whether you should use the natural or one-herd proof or not, would you discourage the large herd owners who would like to have bulls in their herds? Should this be discouraged entirely?

THE CHAIRMAN: This is rather basic, and this, certainly is not an answer to Dr. McGilliard's question, but the basic question is along this line:

What are we seeking in the single herd proof? In other words, is the objective one of devising a scheme for estimating breeding value? Or is it one of producing information on the performance of the daughters of these bulls in this herd, so as to give this particular breeder an indication of how the future performance is going to be in this particular herd?

DR. LEGATES: Well, he is caught on the latter, because his choices are practically nil. To make a comparison, he has got to go across herds to make any choices. I mean, these are the hard facts about it.

DR. BARR: Well, this is a group though.

DR. LEGATES: I beg your pardon?

DR. BARR: We are talking about a group of breeders though.

DR. LEGATES: Yes, but, well, he still has to go to Herd B though, you see, to make his comparisons across herds.

DR. BARR: Yes.

DR. FREEMAN: Well, let me ask this question: excuse me, was it Dr. McGilliard? Were you talking about this, or were you talking about a group of breeders who were exchanging bulls?

DR. MCGILLIARD: Well, I was talking about this, but as they use larger and larger herds --

DR. MEADOWS: Well, let me ask this question: In AI--I think that what you are talking about is selection; what we are talking about is selection; what we are really talking about is choosing among bulls that we have sampled. Now, normally, we don't sample one bull in AI; we sample more than one bull, and then choose among these with, we say, a high degree of accuracy. But we talk about the individual herds, and we try to determine what kind of a bull he has for just one bull. But it seems to me that if he sampled more than one bull, I ought to be able to choose with a high degree of accuracy within a single herd, among those that he did sample in his herd which leads me to Dr. McGilliard's question. Most of them don't have facilities to sample more than two. But if several single herds were likely to combine and sample four bulls--four bulls at the same time--I see no reason why we can't choose among these, particularly if they owned all four bulls. Now if I owned one, and somebody else owned one, naturally, I would give preferential treatment to my bull. And it looks to me like what we should determine is whether we should encourage breeders to sample more bulls, or do you think that AI will be able to sample enough? And if we are going to select them out, should they sample these bulls so that they could choose among what they did sample? I don't see how you could choose among one bull.

That is what I say; this is really what we have been talking about when we ask how accurately are you going to try to estimate his breeding value across a whole population from a single herd. Well, I get the distinct feeling that we may have some trouble distinguishing the breeding value among many bulls across all of the herds. That is what we have been talking about here. These are some of the problems involved.

DR. FREEMAN: Oh, yes, but certainly not to the extent that there is in a single herd.

DR. MEADOWS: No, no, but if he did sample more than one bull at a time, could I choose among what he did sample, however?

DR. FREEMAN: Well, certainly. I don't see why not if there isn't preferential treatment. Now you may not be able to choose among them with as much accuracy, simply because he doesn't have as many daughters.

DR. HENDERSON: If you sample mother-daughter, you get just as much accuracy as AI.

DR. FREEMAN: Certainly. And so really what I think it amounts to is just setting up small AI units out of four or five herds.

DR. MEADOWS: Well, I wonder if operationally, since I am pretty heavily involved in this, do you think that AI is going to sample enough that we want to restrict what they can do at this point, which has some bearing on how much progress we are going to make.

ADJUSTMENTS FOR NUMBER AND DISTRIBUTION OF DAUGHTERS

A. E. Freeman[a]

The discussion since lunch has covered a good deal of what I intended to say. I will try to review and outline the problems, point to areas where work is needed and offer some suggestions.

The numbers and distribution of daughters over herds has been a problem since the beginning of artificial insemination. When substantial numbers of naturally proven bulls were first used in AI service and their AI daughters' production became available, the repeatability of natural service proofs in AI was found to be rather low. Then, the problem of the distribution of a bull's daughters over herds became acute and meaningful.

I am going to go on the premise that if a sire is sampled in artificial insemination, his daughters are distributed such that there is about one in each herd. In our data, this averages about 1.2 daughters per herd. Further, I am going on the premise that such a progeny test forms the basis for a reasonably reliable estimate of what his future daughters will produce. Does anybody want to argue with this statement? Looking at the whole problem, once you depart from this near ideal distribution of essentially one daughter per herd, and where each herd owner has no immediate interest in the bull, then some technology other than what is now in use is needed to make the progeny test a more reliable indicator of the bull's breeding value.

Let's consider some of the possible causes of the lack of repeatability of these proofs. If we consider the lack of repeatability of proofs in a limited environmental situation, such as a single herd, a non-linear increase of daughters over herdmates in different genetic levels could be suspected. That is, the regression of genotypic level on increase of daughters over herdmates is non-linear. I don't think this is a likely cause. The work of Dale Van Vleck showing the regression of daughter on dam to be almost completely linear over a wide range of production is extremely convincing. This work represented rather large numbers of daughter-dam pairs. Further, Van Vleck looked at paternal half-sib estimates of heritability and showed that as the level of production increased, the component of variance due to sires actually increased proportionately slightly more than did the environmental level, which indicated that heritability was perhaps increasing as level of production increased---not markedly, but certainly in this direction. Other evidence could be cited, but the conclusion would be the same. Heritability of milk production seems to be nearly linear over the range in the current population.

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[a] Department of Animal Science, Iowa State University.

[illegible] FOR WORKING [illegible] DISTRIBUTION OF [illegible]

A. E. Freeman[a]

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I [illegible] going to go on the premise that if a bull is sampled [illegible] artificial insemination, his daughters are usually used such that there is about one in each herd. In our data, this averages about 1.2 daughters per herd. Further, I am going on the premise that such a property to [illegible] forms the basis for a reasonably reliable estimate of what his future daughters will produce. Does anybody want to argue with this statement? Looking at the whole problem, [illegible] from this near ideal distribution of associativity one [illegible] per herd, and where each herd owner [illegible] no immediate interest in the bull, then some technology other than what is now in use [illegible] needed to make the progeny test a more reliable indicator of the bull's breeding value.

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[illegible] Oregon State University.

Another possible cause for the lack of repeatability of such sire proofs is that there could be a genotype by environmental interaction.

Looking in the literature for evidence, the estimates of sire by herd-year-season interaction have varied from negative ones up to about seven percent of the total variance. A few estimates may be more divergent than this, but most are in this neighborhood. A point estimate might be two or three percent of the total variance.

This is a fairly small fraction of the total variance, but since the sire component of variance is perhaps of the magnitude of five or six percent of the total variance, the interaction component could, conceivably, be of the same magnitude as the sire component of variance. If you look at genotype-environmental interaction as a source of confusion, so to speak, in sire selection, it could conceivably present some problems.

We and others have done a considerable amount of work on this problem. Most of the previous estimates, including those that we had made, and many others, were made from highly non-orthogonal data. Kelleher, who did his graduate work at Iowa State, selected from DHIA records balanced sets of data consisting of two sires by n herd-year-seasons. By pooling these results he computed the interaction between sires and herd-year-seasons from these balanced sets of data. Obviously, there weren't equal numbers in each subclass, so he randomly chose one out of each subclass and used it. He repeated this five times and obtained point estimates each time. The estimates wer not independent because some subclasses contained only one observation. There were 129 degrees of freedom for sires and 798 degrees of freedom for interaction. The error mean square was computed from the subclasses with multiple observations and had 5,795 degrees of freedom. The magnitude of the error mean square agreed well with the one computed from all non-orthogonal data. By pooling these analyses, his point estimate of the interaction of bulls by herd-year-seasons was about two percent of the total variance. This is the value of 1,520 pounds squared in Table 1, which is based on Kelleher's results.

A meaningful way to look at these results, if you are careful with the interpretation, is to look at the interaction as a possible cause of error in sire proofs. This is what I have intended in the right-hand column, of Table 1. Let me be a little more explicit. If you take the definition of the index (I) of a sire's breeding value, as the average of the intra herd-year-season differences of his daughters from

their contemporaries, then

$\hat{r}_{GI} = \dfrac{\hat{\sigma}_b}{\sqrt{\{\hat{V}(I)\}}}$. The estimated variance of I is

$$\left[1 + \frac{1}{\{\sum_j (1)\}^2} \sum_s \left\{\sum_j \frac{N_{sj}}{\sum_s N_{sj}}\right\}^2\right] \hat{\sigma}_b^2 + \left[\frac{1}{\sum_j (1)} + \frac{1}{\{\sum_j (1)\}^2} \sum_j \sum_s \left\{\frac{N_{sj}}{\sum_s N_{sj}}\right\}^2\right] \hat{\sigma}_{bhs}^2 + \frac{1}{\{\sum_j (1)\}^2} \left\{\sum_j \frac{1}{N_{fj}} + \sum_j \frac{1}{\sum_s N_{sj}}\right\} \hat{\sigma}_e^2 .$$

N_{fj} and N_{sj}, respectively, are the numbers of offspring which the $f^{\underline{th}}$ (test) and $s^{\underline{th}}$ (stablemate) bulls have in the $j^{\underline{th}}$ herd-year-season. σ_b^2, σ_{bhs}^2 and σ_e^2 are the components of variance for bulls, bulls x herd-year-seasons and residual, respectively.

From Table 1, the value for 1 - r_{GI}, representing the best estimate from these data, accounts for about nine percent of the total error in making sire selections.

You will realize that any table of values such as this one depends upon the numbers of daughters, herdmates, bulls etc., that are considered.

I have given only two examples here. Table 2 is less extreme than Table 1 and yet much more restrictive than we find in many true AI situations, where the AI bulls, normally have more than ten daughters in seven herd-year-seasons, but are still distributed with roughly one daughter per herd-year-season. In this case, and many others similar to it, the interaction accounted for only about two percent of the total error involved. If you multiply his point estimate by four, so that it is about 8,000 as an actual value or about ten percent of the total variance, which seems to be as high as could ever be expected, this still only accounts for about six or eight percent of the error in sire selections. Contrasting table 2 to table 1, which might represent something similar to what would

be found in natural service where the sires are used in a very limited number of herd-year-seasons and compared with a limited number of stable-mate sires, this can account for an appreciable part of the total variance.

In summary of this point, within our usual context of sire selection, sire by herd-year-season interactions are an inconsequential source of error in the evaluation of sires whose daughters are distributed over a fairly large number of herd-year-seasons. But, this interaction could be a source of error for bulls that are used in a limited number of herd-year-seasons. In general, the accuracy of selection increases as the bulls are tested in more herd-year-seasons with a fairly large number of stablemate sires, and essentially small numbers of daughters per stablemate sire.

A third possible cause of the lack of repeatability of initial progeny tests with later progeny performance is environmental correlations among progeny or herdmate groups. Table 3 is a summary of some of Dr. McDaniel's work which he graciously consented for me to use. He started with the objective of looking at some of the environmental correlations that are or that may be involved in sire evaluation.

Surely, the problem of environmental correlation among relative groups is one that deserves more investigation. From the available evidence it seems that this is one reason why the initial proof that is made in a limited environmental situation is not highly repeatable in AI. During this conference the causes of environmental correlations and some of the consequences have been discussed. Perhaps I can add to this. You can see from Table 3 that there is some trend for a larger regression or correlation for both milk and fat as the number of herds in which daughters were represented increases. The major increase is after more than one herd is represented. From some of his other work, and I think, also from the same data from which Table 3 was derived, Dr. McDaniel estimated the heritability of milk production to be about .17, and the environmental correlation, the c^2 represents the extra correlation among paternal sisters, contributed by factors other than their sire alone, which paternal sisters may have in common but which may differ from one set of paternal sisters to another.

What is an "appropriate" value for c^2 in sire evaluation? The answer to this is certainly not clear to me. Let's consider some of the other work in the literature. I think that Dr. Van Vleck, in his efforts to find out why his paternal-half-sib and parent-offspring regressions gave different values for heritability estimates -- and

I don't know whether he has really resolved this yet in his own mind--has published some interesting work.

He concluded that the environmental covariance between records of daughters and dams in the same herd was .01 (J. Dairy Sci. 48:1676). In the same publication, they found the environmental covariance between records of maternal-sibs in the same herd was small, but that for full-sibs in the same herd to be important-- from .06 to .12 of the total variance. Later Van Vleck (J. Dairy Sci. 49:195) found the environmental correlation between pairs of half-sibs in the same herd to be .168 and in different herds .086. Considering the effect of environmental correlations in sire evaluation Van Vleck (J. of Dairy Sci. 49:56) concluded from the good agreement of actual and expected correlations between initial and later groups that there is no support for the view that accuracy of prediction in sire evaluation is being over-estimated due to failure to properly account for environmental correlations among contiguous half-sibs in artificial insemination. Other work, such as that of Bereskin and Lush (J. Dairy Sci. 48:356) which I will consider in more detail later, is not so convincing on the latter point. This seems to point out one thing, that the initial progeny test of bulls being sampled for AI should be made with the daughters well distributed over herd-year-seasons. This relates back to some of the earlier discussion here, I believe. At this stage of knowledge, and methodology, it seems that we are not able to handle other situations with a great deal of confidence, so, for now, why not attempt to minimize the problem.

DR. HARVEY: Do you give up on that question?

DR. FREEMAN: Give up on what question?

DR. HARVEY: Give up and just say that there is nothing you can do about it, just give up?

DR. FREEMAN: Oh, no, but it isn't clear how to best evaluate these progeny tests at this point. I think that we can make some beginnings toward it and I will say what I think should be done in a minute. But if you look at Table 4, Bereskin's results, which were published in March, 1965, the difference between the expected and the computed correlations are rather interesting.

In these three studies, the second one, was the only one where the expected and actual correlations were very close. Here he chose equal numbers of daughters randomly from the same herds in the two different proofs. I have no real explanation for the results in study III. In so far as I could see, by discussing this work with him, the way he chose the data should have fairly well approximated on AI situation. You notice that there was not a tremendously large discrepancy between the expected and actual correlation for deviated data using the average of all records for each daughter. This difference appears

[illegible] Dr. Lindzey: It has been really resolved this yet in his own mind.

[illegible] concluded that the environmental correlations between re[illegible] and genes in the same herd was [illegible] (J. Dairy Sci. 46:1646): In the same population, they found the environmental covariance between records of material alike in the [illegible] herd was small, but that for half-sibs in the same herd is to be larger. From .06 to [illegible] the total variance. Later Van Vleck (J. Dairy Sci. 46:1095) found the environmental correlation between pairs of half-sibs in the same herd to be .[illegible] and in different herds [illegible]. Considering the effect of [illegible] correlations in this evaluation Van Vleck (J. of Dairy Sci. 46:[illegible]) concluded from the good agreement of actual and expected correlations between initial [illegible] later groups that there [illegible] support for the view that accuracy of prediction in sire evaluation is being over-estimated due to failure to properly account for environmental correlations among contemporaries half-sibs in artificial insemination. Other work, such as that of Bereskin and [illegible] (J. Dairy [illegible] 46:[illegible]) which I [illegible] consider in more detail later, is not convincing on the latter point. This seems to point out the [illegible] the initial progeny test of bulls being sampled for AI should [illegible] with the daughters well distributed over herd-year-seasons. [illegible] relates back to some of the earlier discussion here, I believe. As this stage of knowledge, and methodology, it seems [illegible] we are not able to handle other situations [illegible] a great deal of confidence. So, for now, why not attempt to minimize the problem.

DR. HARVEY: Do you give up on that question?

DR. [illegible]: Give up on what question?

DR. HARVEY: Give up and just say that there is no? As you said about it, just give up?

DR. [illegible]: No, but it isn't clear how to best evaluate bulls progeny tests at this [illegible]. I think that we can make some beginning toward it and [illegible] what I think should be done in a minute. But if you look at Paul [illegible] Bereskin's results, which were published in March, 1957, [illegible] difference between the expected and the computed correlations are rather interesting.

[illegible] one, then the [illegible] one were [illegible] close. [illegible] the other [illegible] two herds herds [illegible] the [illegible] different [illegible] on the results in a study [illegible]. In [illegible] this work with him, the way he [illegible] well approximated on AI situation.

larger using only first records. I don't really know why.

Another indication that points in the direction of environmental correlation among paternal half-sibs has consistently shown up on our data. If we look at nearly any sort of estimates based on half-sib components, they aren't very meaningful unless they have been made from sires who had daughters in several herds. I chose Table 5 to indicate this. You can see, for instance, the estimated heritability of deviation milk when a sire was used in at least two herds, was .41. When sires daughters were in more herds the estimates declined until they appear stable at about fifteen herds, although the largest change is made by the time sire daughters are in at least four herds.

Perhaps we could summarize the most pressing problems in this area as follows. The first is a single herd proof, and I think that enough has been said about this. The second is where the sire has been progeny tested partly in a single herd and also has AI daughters in his initial progeny test. This is perhaps less common that it was a few years ago, where the bull may have been purchased from a breeder after he was about breeding age, and after he had bred a number of heifers in that herd. So, essentially, it is a single-herd-AI mixed situation. The other is a very old bull with a large number of daughters, where there has been an opportunity for a great deal of selection among his daughters. Then, primarily for special mating purposes, it may be necessary to compare him against a younger bull whose first progeny test is available and is based on relatively unselected first calf heifer records. There certainly are problems in making judgements between these bulls. This is over simplifying the total problem, because any time a new bull is considered for replacing one already in the stud, the decision of which sire to sell must be made regardless of the type of information available.

Ideally, it seems desirable to have a sire evaluation procedure which will take into account numbers of daughters, the distribution of daughters over herd-year-seasons, the number of herdmates, the number of herdmate sires and perhaps other considerations so that all sires can be ranked with some confidence regardless of the type of information available. More research is certainly needed in this area.

But, even now shouldn't we be using some value of c^2, or something of this nature, to evaluate the single herd proof or those in a limited number of herds?

The net effect of doing this is that you give less weight to the same number of daughters when they all produce in a single herd as opposed to being distributed over many herds. When the distribution of the daughters is limited, the correlation between a bull's breeding value and a weighted function of the daughter-herdmate difference tends to plateau rather quickly and never reaches a limit of 1.0.

Regressions such as [2] or [6] in Bereskin's paper (J. Dairy Sci. 48:356) involving C^2 could be used for single herd proofs. From the above discussion, it isn't clear what value for c^2 should be used. In fact, it is likely to depend on the distribution of daughter, etc. If single herd progeny tests are evaluated this way, it seems they should be listed separately from A.I. progeny tests when made available to the public to call attention to the different type of information and to show less confidence in the estimate of the bulls breeding value when estimated this way. I have purposely not gone into detail on the specific equation that could be used with single herd progeny tests. The regressions can easily be derived with expectations of linear forms and they will differ depending upon the model chosen. We have not thoroughly investigated this problem, so detailed suggestions would not be appropriate. I do think that the numbers and distributions of daughters and allied considerations in progeny tests deserves thorough investigation.

Dr. Corley, I didn't add as much to the discussion as I would have liked, but most of the evidence is rather fragmented.

DISCUSSION

THE CHAIRMAN: Any comments or questions that you have of Dr. Freeman?

DR. HENDERSON: How much of that correlation in the same season is trouble with age factors, assuming the AI calves are all in the same season, and lactation time -- and being compared to herdmates for varying ages? This could contribute a great deal to this, but maybe not all of this.

DR. FREEMAN: It certainly could but I have no precise answer to your question. This could be looked at by selecting data. The validity of this is perhaps questionable but one could limit such comparisons to animals of about the same age that are in different herd units.

DR. BARR: I don't know; from an entirely judgement standpoint, would it be better to recommend that this particular group of young sires from which you select be evaluated using a c^2 value?

DR. FREEMAN: That depends on what you wanted to do with them. If you limited the comparison or the choices to only among those that were sampled in that herd-year-season and are to be used back in the same herds, perhaps yes.

But, if you were going to make choices between these and others that weren't sampled that way, no.

DR. HENDERSON: It would be the worst way.

DR. BARR: Well, not entirely, because I don't think choices are ever made in exactly that way.

DR. FREEMAN: That is true. I think this would be asking for too much trouble, because it would be too much temptation to use the sire evaluation in some way other than it was intended.

DR. LAND: This creates real problems when you go to compare this year's group of bulls with a sample of those last year. That would make this decision invalid.

DR. BARR: If you are planning on sampling, it may turn out that none of these bulls are good enough.

DR. GAUNT: Yes, it is possible. It happens.

DR. FREEMAN: So it seems to me that you are always making a choice among those young bulls whose progeny information is just available and what is in the stud at the time.

DR. HENDERSON: In other words, do you bring all of them or any of them, and what fraction -- any of them or all of them or what part? This is weighed against what you already have. At least, that is what it should be, but it is difficult.

DR. BARR: It is pretty costly.

THE CHAIRMAN: With our present system, should we be giving any consideration toward the possibility of taking into account distribution of herds in the so-called AI proof or multiple herd proof?

DR. HENDERSON: Well, this is what I will talk about tomorrow -- whether or not we should, I can answer better tomorrow.

THE CHAIRMAN: You mean, defer that question until tomorrow. I will also ask another question that has been talked about: Should any consideration be given to the feasibility or the possibility of adjusting the winthin-herd proof as a means of estimating breeding values?

DR. GAUNT: What are you going to adjust it for though?

DR. BARR: Adjust it for what?

DR. FREEMAN: Numbers of daughters.

DR. GAUNT: You have to have some basis for adjustment.

THE CHAIRMAN: In other words, you are saying no.

DR. HENDERSON: I am saying yes; I am saying yes if we can get a fair comparison, ignoring preferential treatment between a natural service bull and the AI population.

DR. FREEMAN: But, Dr. Henderson, from a practical standpoint, do you think that we should ignore this? Maybe that is the other really practical question. I have got to be convinced that we can ignore preferential treatment.

DR. HENDERSON: Well, I think that probably two separate listings would be better.

DR. TOUCHBERRY: But in a separate listing, you are still faced with the same problem, arent't you?

DR. HENDERSON: Yes.

DR. TOUCHBERRY: You still have to make a decision, I think.

DR. HENDERSON: Of course, the question is, when people are going to use natural service bulls -- we have the obligation to provide them with the best possible.

DR. TOUCHBERRY: Yes.

DR. HENDERSON: And should we ignore the question and say that we won't provide you with anything?

DR. YOUNG: With regard to this table on page 2, some breeders are interested in putting bulls out and getting their proofs in a small number of herds; does this mean that it would be just as well to put a bull in two herds as in ten?

DR. FREEMAN: Why don't you ask Dr. McDaniel this? This is his data.

DR. McDANIEL: Well, if you look, you will see that these correlations bounce about quite a bit. When you come down here to where you start getting the numbers, and you have got five herds, four herds, then you have a lower regression. Actually what we did is work out the environmental correlation, assuming that our method was right, taking each of these measures, and we came up with a simultaneous solution for c^2 and h^2. According to these results, you would need to go to as many herds as you could possibly get. One daughter per herd would be ideal.

And now the reason that I showed these tables is that you can get the correlations and regressions in different samples.

DR. YOUNG: But the values are quite similar, from two to ten, after going up, frequently, one to two.

DR. McDANIEL: Well, the largest regression in it is significant; it is almost a value of about 1.5; you can work it out.

Actually, I had twenty-seven different equations here, that were split down to where you had six daughters in one herd, and each of the others in a single herd, and so forth. And actually, the h^2 and the c^2 values came from that. And how if you take a bunch of bulls that have daughters in five herds, and work out the different distributions, the regression is in a very similar direction.

DR. MEADOWS: I have one question about the data: Were these data peculiar to those who just had two herds represented? Or were these a sampling of two among many?

DR. McDANIEL: No. actually, these --

DR. MEADOWS: Or just three?

DR. McDANIEL: No

DR. MEADOWS: Just three available?

DR. McDANIEL: We took data and from a group of AI daughters.

DR. MEADOWS: Yes.

DR. McDANIEL: And sorted them by herds.

DR. MEADOWS: Yes.

DR. McDANIEL: In other words, such that they were known.

DR. MEADOWS: Well, maybe I didn't make my point clear. You see, if you have a syndicate or something, that is breeding a bull, and he is being used in two herds then --

DR. McDANIEL: No.

DR. MEADOWS: That is different from the thing that we are looking at here. So we still don't have the --

DR. McDANIEL: This kind of thing gets more random.

DR. MEADOWS: That is the reason that I was surprised that you didn't have a greater correlation of differences as you dropped off the small herd, and I suspect that in syndicates that we are talking about, where the bulls are used and those groups know the bulls, that your effect of herd size would be somewhat --

DR. McDANIEL: No, what I was looking at here would be just the AI situation, where some areas have two and three and four daughters per herd, and I was not looking at the situation that you are talking about. This is strictly AI data.

THE CHAIRMAN: I would like to direct a question to Dr. Barr. Do you feel that it is important that more research be done to better determine the usefulness of dam information, as a possible contribution to within herd proofs?

DR. BARR: You mean, from a practical standpoint, with respect to bias? Or do you mean with respect to accuracy of predicting breeding value? For the first one, I would say probably yes. For the second one, I would say probably no.

THE CHAIRMAN: Well we assume that we can estimate breeding values; let us say, with our present USDA programs, where we are computing unadjusted differences, the daughter-herdmate deviations in a single-herd proof. Do you think that there is a need for additional research to better determine the advisability of considering dam information as a part of this evaluation scheme?

DR. BARR: I would like to see if it would be possible to generate, with the data that we now have -- to generate a situation we think might happen in the future, with daughter-herdmate comparisons, and single herds. And let us say that we are talking about a selected segment of the herds. I probably shouldn't say "selected", but unique set of herds. So we can look at this on a population basis, and I think that it is pretty apparent that it really doesn't warrant the effort, but until we can see the situation that can exist -- I am -- let's face it, talking about registered herds that have dealt with daughter-dam comparisons for years. Now what happens to them when they find out that a daughter-herdmate comparison is the official method for sire proving for their particular breed sources? Can we, with the data that we now have, generate the kind of conditions that might occur under this situation? If we can, then probably we ought to look into it. I don't think we can. I haven't made myself very clear, have I?

THE CHAIRMAN: Well, I doubt it. Does anybody else want to talk?

DR. FREEMAN: I would like to make a statement about what Dr. Henderson said a while ago in terms of using single herd proofs. It seems to me that we will continue to have sire proofs made in the single herds. Furthermore, it seems we should do all we can to estimate a bull's breeding value accurately as possible from these data. Also, unless there is something of which I am unaware, this is not likely to be accurate enough to use these bulls, based on single herd proof, in an unlimited AI situation. If we can improve the estimates of breeding value for the single herd progeny test and give a breeder some help, fine. But we shouldn't kid ourselves into thinking that such estimates are accurate enough to justify using these bulls extensively in AI, unless this is shown to be true.

DR. MEADOWS: The adjustments you are referring to are number of daughters and level of AI?

DR. FREEMAN: Yes.

DR. HENDERSON: And an age factor, based on season differences.

THE CHAIRMAN: Have we suggested as yet any biometrical approaches toward trying to cope with preferential treatment or selective mating? I haven't detected any, but I wondered if anybody is suggesting any at this point.

DR. HENDERSON: Well, on the selective mating, it probably isn't too bad if one evaluates the mate on the basis of the information you have on her; but as for preferential treatment, I don't see how you get at it that way.

DR. TOUCHBERRY: If it relates to certain daughters, you can get at that. To evaluate preferential treatment, you would have to be familiar with the situation.

DR. BURNSIDE: I don't think that it can be done without going into these herds and attempting to classify them in some way. We are attempting to classify herds in a number of ways in Ontario -- purebred and grade herds, and one of the things that interests me is a classification on mating procedures where we are attempting to single out the purebred herds that are using as a part of their breeding program a good young bull. I think that if there is preferential treatment, this is where it may happen. And we are rather interested in sire by herd interactions, so we classify them this way. I am not sure that it will be 100 percent that we will get under these circumstances.

DR. FREEMAN: Well, let me ask a question. Why aren't we using some regression to adjust for numbers daughters that includes a c^2 term? One of this form: $\frac{nh^2}{4 + (N-1)(h^2 + 4c^2)}$. I can remember this one, but we probably should use one based on a more realistic model. It seems that some thing of this nature is certainly better than what we are now doing.

The reason I brought this up again is to stimulate some discussion on its use.

DR. TOUCHBERRY: I think that what you are saying there is where you proved the bull in one herd, and you are going to use him across the board --

DR. FREEMAN: Right.

DR. TOUCHBERRY: Then c^2 is certainly going to be much larger than it is if you proved the bull in one herd, and continue to use the bull there.

DR. FREEMAN: That's right, and if you were going to use him across herds, and you used a relatively large value for c^2 -----

DR. TOUCHBERRY: Yes.

DR. FREEMAN: You are never going to get his estimated breeding value very high anyway.

DR. TOUCHBERRY: And if you look at all of the herds --

DR. FREEMAN: Yes.

DR. TOUCHBERRY: And all of these little things, and you find that the c^2 term is quite large, which is one reason that I say that we should go ahead and list these bulls and rank them, because I think that this also brings home just how useless sometimes a one-herd proof is when we try to extend it across the board.

DR. FREEMAN: Now, if you want, you can build into this equation the number of herdmate bulls that were involved in the comparison, and so on. It seems to me that something like this ought to be done, at least, as a first step.

DR. TOUCHBERRY: The same is true with the daughter-dam comparison.

DR. FREEMAN: Yes.

DR. TOUCHBERRY: You can think of that.

DR. FREEMAN: Yes.

THE CHAIRMAN: Any other questions?

DR. McGILLIARD: I think that this one of preferential treatment is a pretty hard one to deal with, because what is preferential treatment? You feed your cows according to production and it could be you feed them all the same amount. Is our current system preferential treatment?

DR. TOUCHBERRY: I don't believe that there is quite as much to that as we lead ourselves to believe at this time. I think that there is too much emphasis on the general herd average, and having a high level all through the herd. I don't think that we could feed on such a tremendous amount of preferential treatment.

DR. PLOWMAN: Well, there are very few places that limit roughage to cows, and so cows all have the same opportunity to eat roughage. And so even if you give the cow an extra pound of grain, she is not going to eat quite as much roughage.

DR. TOUCHBERRY: Yes.

DR. PLOWMAN: So on the total herd basis, it is pretty hard to treat a group of cows different than the others.

DR. TOUCHBERRY: Yes, but one cow you can pull out though.

DR. PLOWMAN: Yes, but this takes special effort, real special effort, and these sorts of things you can find more easily. You can go into the herd and find them more easily than small ones.

DR. TOUCHBERRY: Well, now he says don't be so naive! I don't think it is as widespread, however.

MR. RUMLER: You are still breeding individual animals.

DR. McGILLIARD: A man who owns a bull has an axe to grind.

MR. RUMLER: May I ask a question?

THE CHAIRMAN: You may.

MR. RUMLER: Am I correct in assuming that from the questions that we have heard here this afternoon, that so far, at least, we are genetically incapable of evaluating a bull used in a single herd or two or three herds? This is the conclusion that I would draw from the discussion; is that right?

DR. PLOWMAN: Well, for what purpose?

DR. HARVEY: No, just compare them across the board.

DR. FREEMAN: The whole thing really goes back to design. If there is something that is built into it that isn't straightforward--

DR. HARVEY: This can be done to put it in line with the herds. This has been done in poultry random sample tests for many years, and stock testing in one location, compared to stock testing in all locations, is being done routinely, and has been done for several years, and the same thing can be done for dairy cattle.

DR. BENSON: We are going to have some unhappy breeders, if you start testing and adjusting Non-AI.

DR. LEGATES: There you also have some estimate of the reliability of your sample, too, that isn't recognized by the ordinary layman -- in other words, he looks at just the breeding value; they may be the same magnitude and have quite different reliability.

DR. HARVEY: The standard errors.

DR. LEGATES: Yes.

DR. HARVEY: Educate them.

THE CHAIRMAN: Bob, I would like to encourage you to comment and speak not as a guest but as a member of the group -- for whatever membership is!

DR. TOUCHBERRY: We don't believe in preferential treatment!

THE CHAIRMAN: Dr. Barr, did you raise a question in your presentation as to what about pedigree methods for evaluating these bulls within herds? Would you amplify that a little?

DR. BARR: Well, there is a very interesting thing here on this table. Item B, we calculate correlations by the pedigrees with fairly complete figures on bulls and AI proof, and I think that the hypothesis was made at that time that the pedigree was worth from eight to ten daughters. If you really want to be critical about it, what is the average number of daughters in one-herd proofs? Certainly not much greater than ten.

DR. McGILLIARD: But that comes on top of the pedigree.

DR. LEGATES: Yes, but we have other things. These were selected from a whole generation. And you have this five-year trend, and you have to have this big superiority, and it is in your favor, provided you are moving upward.

DR. FREEMAN: But that should have been built into what Dr. Barr did in this eight or ten daughters, because he was looking at it in retrospect.

DR. MEADOWS: Yes, he was, but the whole population from which those were drawn was more than the population of the pedigree, but I was saying in practice.

DR. BARR: In practice.

DR. MEADOWS: I was saying in practice.

DR. BARR: It wasn't realistic in terms of --

DR. MEADOWS: I said you indexed these dams, and I mean you used new ways to do this, and currently this is not being done, or hasn't been done the same way by the individual breeder. It can be done, but I say it hasn't been done.

DR. BARR: In terms of these c^2 values, for this same Holstein data, we obtained a heritability by parent-offspring regression of about .24; and then I went back and said, all right, assuming that this is the best estimate of the c^2 here, it would be zero, so this really represents the heritability.

DR. McGILLIARD: What is that?

DR. BARR: Parent-offspring regression on the same data, adjusted.

Table 1

Loss of accuracy in sire selection because of a sire x herd-year-season interaction where the test-bull and each of two stablemate-bulls have 10 daughters each in a single herd-year-season.
(Kelleher Ph. D. Thesis)

Value of $\hat{\sigma}^2_{bhs}$		Additional decrease in r_{GI} due to $\hat{\sigma}^2_{bhs}$	
Absolute value	Expressed as % of total variance	Actual value	Expressed as % of $1 - r_{GI}$
0	0	0	0
1,000	1.35%	.033	6.73%
1,520	2.03%	.048	9.48%
2,000	2.66%	.061	11.68%
3,000	3.93%	.085	15.50%
4,000	5.17%	.105	18.55%
5,000	6.39%	.123	21.04%
6,000	7.57%	.139	23.12%
7,000	8.72%	.153	24.89%
8,000	9.60%	.166	26.41%

Table 2.

Loss of accuracy in sire selection because of sire x herd-year-season interaction where an A.I. bull, which has 10 daughters in seven herd-year-seasons

Values of $\hat{\sigma}^2_{bhs}$		Additional decrease in r_{GI} due to $\hat{\sigma}^2_{bhs}$	
Actual value	Expressed as % of the total variance	Actual decrease	Decrease expressed as % of $1 - r_{GI}$
0	0	0	0
1,000	1.3%	.005	1.16%
1,520	2.03%	.008	1.73%
2,000	2.66%	.011	2.25%
3,000	3.93%	.016	3.29%
4,000	5.17%	.021	4.29%
5,000	6.39%	.026	5.23%
6,000	7.57%	.030	6.13%
7,000	8.72%	.035	6.99%
8,000	9.60%	.039	7.81%

Table 3.

RELATIONSHIPS BETWEEN INITIAL GROUP OF 10 PROGENY AND LATER SET OF 120 WHERE DIFFERENT NUMBERS OF HERDS WERE REPRESENTED IN THE INITIAL PROGENY GROUP
(Ben McDaniel)

Number of herds represented	Number of progeny groups used	Correlations		Regressions	
		Milk	Fat	Milk	Fat
1	30	.20	.31	.084	.136
2	78	.59	.58	.304	.300
3	185	.52	.48	.334	.309
4	274	.49	.50	.279	.278
5	424	.47	.50	.289	.294
6	530	.50	.50	.312	.309
7	571	.52	.48	.308	.282
8	495	.49	.46	.282	.260
9	393	.50	.49	.308	.288
10	212	.59	.51	.336	.300

Estimated: $h^2 = .17$
$c^2 = .10$

Ben Bereskin. J. of Dairy Sci. Mar. 1965

Study I Proof 1 - Daughters random, from high level herds.
Proof 2 - Daughters random, from low level herds.

II Proof 1, Proof 2 — Equal numbers of daughters from same herds.

III Proof 1, Proof 2 — Herds randomly selected, daughters randomly selected, no repeats.

Table 4. Sample (r) and expected ($\hat{r}$) correlations of separate proofs for bulls

	No. of bulls	First available record		Av of all records for each daughter	
		Nondeviated	Deviation	Nondeviated	Deviation
Study I	60				
r		.17	.23	.24	.30
$\hat{r}$		.57	.63	.57	.63
Study II	61				
r		.77	.65	.80	.67
$\hat{r}$		.55	.61	.55	.62
Study III	58				
r		.20	.30	.31	.40
$\hat{r}$		.56	.62	.56	.62

Table 5

Estimates of heritability by paternal half-sib analysis of variance using all DHIA records with sire identification (Butcher Ph. D. Thesis)

	Lactation 1	Lactation 2	Lactation 3
only sires used in at least two herds			
h^2 deviation milk	0.415 ± .034	0.310 ± .040	0.187 ± .049
h^2 deviation fat	0.389 ± .033	0.431 ± .043	0.406 ± .070
No. of sires	430	258	134
Within sire d.f.	11,352	5,432	2,194
only sires used in at least four herds			
h^2 deviation milk	0.377 ± .404	0.266 ± 0.44	0.180 ± .053
h^2 deviation fat	0.355 ± .038	0.394 ± .056	0.386 ± .080
No. of sires	234	141	79
Within sire d.f.	9,108	4,379	1,834
only sires used in at least ten herds			
h^2 deviation milk	0.354 ± .050	0.215 ± .045	0.148 ± .054
h^2 deviation fat	0.338 ± .049	0.372 ± .063	0.405 ± .103
No. of sires	107	71	42
Within sire d.f.	7,881	3,806	1,537
only sires used in at least fifteen herds			
h^2 deviation milk	0.351 ± .060	0.213 ± .051	0.140 ± .058
h^2 deviation fat	0.342 ± .059	0.379 ± .073	0.407 ± .117
No. of sires	78	52	29
Within sire d.f.	7,384	3,485	1,359

POPULATION AND SAMPLE SIZES NEEDED

R. W. Touchberry[a]

Up to now most of the discussion has been on adjusting production records for genetic trends, extending incomplete records to a complete basis, and correcting for the selection of records. In the material I will present it has been assumed that the records are age corrected and complete and that the individual records are weighted equally. This isn't as naive as it sounds because after extending or adjusting records they are usually treated in this manner.

The main point I want to project is that in testing dairy sires we should be satisfied with fewer daughters per sire, but test more young sires. To substantiate this argument it is necessary to develop certain algebraic expressions for the regression of the breeding value of the sire on different sire indices and to show how these regression coefficients are used in deriving the genetic gain expected from selection among the sires proven. Further, the standard errors of the regression coefficients will be derived to demonstrate the "reliability" of the different indices and to contrast the "reliability" of AI and natural proofs.

The breeding value of the top $\underline{b}$ per cent of the sires evaluated would be expected to exceed the mean breeding value of all sires evaluated by the amount,

$$(\Delta G_s) = b_{G_s I} z/b \; \sigma_I$$

where $b_{G_s I}$ is the regression of the breeding value of the sire (G_s) on the index I, z/b is the mean of the top $\underline{b}$ percent of the standard normal distribution, and σ_I is the standard deviation of the index involved. The above formula can be written in terms of the correlation between the breeding value of the sires and the index as follows:

$$\Delta G_s = r_{G_s I}(z/b) \; \sigma_{G_s}$$

Thus, the amount the expected breeding values of the top b percent of the sires exceeds the mean expected breeding value of all aires evaluated is proportional to the correlation between the breeding value of the sires (G_s) and the index (I) used to predict the breeding value. When selection

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is for one trait, σ_G is a constant regardless of what index is used; thus $r_{G_s I}$ is a convenient expression for comparing various sire indices.

Assuming that mating is random, that the daughters are a random sample of daughters, that the stablemates of each daughter are a random sample of the cows in the herd, that a sire has only one daughter per herd, that each daughter has K stablemates, and that only one of the sires being evaluated has a daughter in any one of the herds involved, the regression of the breeding value of the sire (G_s) on the average of N daughter-stablemate comparisons $(0 - \overline{C}_K)_N$ is:

$$\text{(I)} \quad b_{G_s \overline{(0 - \overline{C}_K)}_N} = \frac{2\,NKh^2}{K(N-1)h^2 + 4(K+1)\,(1-S) + 4(K+1)\,(N-1)\,(1-S)e^2}$$

In formula (I), N is the number of daughters, K the number of stablemates per daughter, h^2 is heritability, S is the correlation between stablemates and between daughter and stablemates, and e^2 is the environmental correlation between the daughter-stablemate deviations for a sire.

The correlation between the breeding values of the sires (G_{s_i}) and the means of the daughter stablemate comparisons $\overline{(0_i - \overline{C}_i)}$ is:

$$\text{(II)} \quad r_{G_s \overline{(0 - \overline{C}_K)}_N} = \sqrt{\frac{NKh^2}{K(N-1)h^2 + 4(K+1)\,(1-S) + 4(K+1)\,(N-1)\,(1-S)e^2}}$$

The conditions specified for deriving the above regression and correlation coefficients tend to maximize these coefficients for a given N and K. In a sense formulas (I) and (II) represent the maximum accuracy in predicting the breeding values of sires for use in AI. At the other extreme is the case where all of a sire's daughters are in one herd.

A second index usually referred to is the daughter average ($\bar{O}_N$). If all the assumptions for deriving the daughter-stablemate comparison are again used except those concerning stablemates, it can be shown that the correlation between the breeding value of the sire G_s and the average of $\underline{N}$ daughters $\bar{O}_N$ is:

$$\text{(III)} \quad r_{G_s \bar{O}_N} = \sqrt{\frac{Nh^2}{4 + (N-1)h^2 + 4(N-1)e^2}}$$

The regression of the breeding value of the sire G_s on the average of $\underline{N}$ daughters $\bar{O}_N$ is

$$\text{(IV)} \quad b_{G_s \bar{O}_N} = \frac{2Nh^2}{4 + (N-1)h^2 + 4(N-1)e^2}$$

In both formulas $\underline{N}$ is the number of daughters, $\underline{h}^2$ is the heritability of the trait involved and $\underline{e}^2$ is the environmental correlation between the single records of the $\underline{N}$ daughters of a sire.

A third index frequently used is the daughter dam comparison. By making the same assumptions as were made regarding the daughter stablemate comparison except for those referring to stablemates and random mating, the correlation between the breeding value of the sire G_s and the average of the single records of N daughters minus the average of the single records of $\underline{N}$ dams ($\bar{O}_N - \bar{D}_N$) is:

$$\text{(V)} \quad r_{G_s(\bar{O}_N - \bar{D}_N)} = \sqrt{\frac{Nh^2}{8 + (N-5)h^2 + 4(N-1)\ (e^2 + w) - 8U - 8(N-1)V}}$$

The regression of the breeding value of the sire (G_s) on the average of the single records of $\underline{N}$ of his daughters minus the average of the single records of their $\underline{N}$ dams is:

$$\text{(VI)} \quad b_{G_s(\bar{O}_N - \bar{D}_N)} = \frac{2Nh^2}{8 + (N-5)h^2 + 4(N-1)\ (e^2 + w) - 8U - 8(N-1)V}$$

In the above formulas $\underline{h}^2$ is heritability, $\underline{N}$ is the number of daughters and also the number of dams, $\underline{e}^2$ is the correlation between the daughters of a sire resulting from a common environment or because their dams are relatives, $\underline{w}$ is the correlation between the mates of the sire (both genetic and environmental), $\underline{U}$ is the correlation between a dam and her daughter and $\underline{V}$ is the correlation between one mate and the daughter of another mate of the sire.

Shown in Tables 1, 2, 6, and 8 are numerical values of the correlations between the breeding value of a sire and the three different indices. By examining these correlations it is apparent that the daughter stablemate comparison is slightly superior to the other two indices for the conditions assumed. It is further apparent that a small environmental correlation between the daughters of a sire, the daughter stablemate differences, or the daughter-dam differences, markedly reduces the correlation between the breeding value of the sire and the respective index. In this respect it is probable that $\underline{e}^2$ will have a larger value for the daughter average or the daughter-dam difference than for the daughter-stablemate comparison; thus the daughter-stablemate comparison is probably more superior to the daughter average and the daughter-dam comparison than is shown in Tables 1, 2, 6, and 8.

From Tables 1 and 2 it is apparent that little gain in accuracy results from having more than five stablemates per daughter. In the national DHIA data the average number of stablemates per daughter is greater than five. This is a reassuring property of the daughter-stablemate comparison as an index.

The correlation between the breeding value of the sire and any one of the three indices is 0.80 or larger when as many as fifty daughters are included in the index. Utilizing the fact that the genetic superiority of the sire (ΔG_s) is $r_{G_s I}(z/b)\sigma_{G_s}$ it can be seen that there is little to be gained by continuing to refine the estimate of $r_{G_s I}$ by increasing the number of daughters per sire. Further, as the number of daughters per sire increases, z/b decreases if there is a limited number of matings a stud can make in testing young bulls.

Let's assume that for one breed a stud can afford to mate enough cows to young unproven sires to result in 1,000 daughters per year with

$\underline{E}^2$ a heritability, $\underline{I}$ is the number [illegible] also the number of sires, $\underline{S}$ is the correlation between the daughters of sires resulting from a common environment or because their sires are [illegible] $\underline{Y}$ is the correlation between the mates of the sires (both sexes [illegible] one 1), $\underline{U}$ is the correlation between a [illegible] her daughter and $\underline{V}$ is the [illegible] between [illegible] mate and the daughter of another mate of the sire.

Tables 1, 2, 6, and 8 are numerical values of the correlating [illegible] the [illegible] value [illegible] a sire and the three different indices. [illegible] It is apparent that the [illegible] establemate comparison is slightly superior to the other two indices [illegible] the conditions assumed. It [illegible] apparent that a small environmental correlation between the [illegible] of a sire, the daughter establemate difference, or the daughter [illegible] differences, markedly reduces the correlation between the breeding value of the sire and the respective index. In this respect it is probable that $\underline{c}$ will have a larger value for the daughter average or the daughter-dam difference than for the daughter-establemate comparison; thus the daughter-establemate comparison probably more superior to the daughter average and the daughter-dam comparison than is shown in Tables 1, 2, 6, and 8.

From Tables 1 and 2 it is apparent that little gain in accuracy results from having more than five establemates per daughter. In the national LHIA data the average number of establemates per daughter is greater than five. This is a reassuring property of the daughter-establemate comparison as an index.

The correlation between the breeding value of the sire and any one of the three indices is 0.80 or larger when as many as thirty daughters are included in the index. Utilizing the fact that the genetic superiority of the sire (ΔG_s) is $r_{G_s I}(2/\delta)\sigma_{G_s}$ it can be seen that there is little to be gained by continuing to refine the estimate of $r_{G_s I}$ by increasing the number of daughters per sire. Further, as the number of daughters per sire increases, $2/\delta$ decreases if there is a limited number of matings a sire can make in testing young bulls.

Assume that for one breed a sire can sire enough [illegible] mate enough [illegible] sires to result in 1,000 daughters per year with

complete records. The remaining cows serviced by the stud will be mated to older proven bulls. Further assume that the stud should add 5 progeny tested bulls per year to its battery of older bulls. The stud may follow a number of alternatives in choosing the five bulls per year, but for each alternative it is assumed that the stud has made special matings to produce a sufficient number of young bulls for testing. The stud may decide to purchase only enough young bulls resulting from the special matings to be assured that five young bulls will be available to add to the stud each year. In this case the stud would have wasted the potential genetic gain resulting from using the 1,000 test daughters and the realized genetic gain would depend entirely on the soundness of the selective mating program and chance. Such a program would have the advantage of avoiding the expenses concomitant with purchasing, keeping and testing more young bulls than are needed to add to the stud each year.

The stud could be more progressive and utilize the 1,000 test daughters to progeny test a number of young bulls. In choosing this alternative the question arises as to how many young sires should be tested per year. Shown in Table 9 are values of z/b for choosing 5 bulls out of 10, 5 out 20, etc. The values for z/b when the number of bulls ranged from 10 through 50 were calculated from the appropriate values in Table XX of Fisher and Yates. When 100 and 200 bulls were tested, the z/b values came from the areas and ordinates of the normal curve. The third line of Table 9 is a relative comparison of the expected genetic superiority of the 5 young sires chosen over the mean of all young bulls tested. There were 100, 50, 40, 25, 20, 10, and 5 daughters per tested sire when 10, 20, 25, 40, 50, and 100, and 200 sires were tested. The third line of Table 9 stresses the fact that most AI organizations should be testing more young sires on a basis of fewer daughters per sire and doing a more rigorous job of culling those young sires that prove to be inferior on a basis of the stablemate comparisons. All young bulls tested still result from carefully planned matings thus utilizing to the fullest the pedigree information.

An important point concerning Table 9 is that approximately the same relative genetic superiority results when anywhere from 20 to 50 young sires are tested on a basis of from 50 to 20 daughters per sire. Under the conditions specified here, the stud should test at least 20 young sires per year but not more than 40.

The added expense of producing, obtaining, keeping, and testing a large number of young sires that may not be used suggests that from an economic standpoint the stud will probably settle for testing 20 to 30 young bulls. Testing 20 young bulls from which only 5 will be chosen is probably beyond the realm of most studs. In this respect it seems that

most studs could markedly reduce the costs of purchasing young bulls by a more logical contract agreement. Why couldn't the stud purchase all young bulls at a flat rate of $250 per bull on the stipulation that the seller would receive additional compensation on a basis of the daughter stablemate comparison and the number of cows serviced by the bull? Such a system would tend to increase the payment for bulls that are really good and decrease the frequency of paying large sums of money for an untested, big name bull.

The information in Tables 1, 2, 6, 8, and 9 indicates that the greatest opportunity for increasing genetic progress is to test more young bulls than is now the practice. To do this we must be satisfied with a less accurate test on the individual young bull. It is my opinion that we should be working to devise plans whereby a much larger number of young bulls can be tested economically rather than striving for the ultimate in adjusting and extending records. The greatest potential genetic gain is in testing more young sires.

If one is to settle for a progeny test based on approximately 25 daughters the question of reliability of the predicted breeding value of the sires is of importance.

The variance of the predicted breeding value of a sire may be written as:

$$\text{(VII)}\quad \sigma^2_{\hat{G}_s} = h^2 \sigma^2_p \left(1 - r^2_{G_s I}\right) \left\{\frac{N_s + 1}{N_s}\right\} + (I_s - \bar{I})^2 \sigma^2_{b_{G_s I}}$$

In the above expression $\underline{h}^2$ is the heritability of the trait involved and σ^2_p is the variance between animals each having a single record of the trait. If the young sires tested are the result of pedigree selection and special matings it is probable that the variance of the breeding values of the sires is less than $h^2\sigma^2_p$. I is the index used to measure the breeding value, N_s is the number of sires tested, $r_{G_s I}$ is the correlation between the breeding value of the sire and the index, and $b_{G_s I}$ is the regression of the breeding value of the sire on the index.

The first term of the variance of the expected breeding values contains the factor $\frac{N_s + 1}{N_s}$. As N_s changes from 25 to 100 the factor $\frac{N_s + 1}{N_s}$ changes from 1.04 to 1.01; thus, it is apparent that any marked reduction in the variance of the exprected breeding values resulting from increasing N_s must come from the factors $(\sigma^2_{b_{G_s I}})$, $(1 - r^2_{G_s I})$. and $(I - \bar{I})^2$.

The standard errors $(\sigma_{b_{G_s I}})$ of the regression coefficients of the breeding value of a sire on the various indices are as follows:

$$\text{(VIII)}\quad \sigma_{b_{G_s(\overline{O-C_K})_N}} = \left[\frac{1}{\sqrt{N_s - 1}}\right] \cdot \left[\frac{\sqrt{4KNh^2\left[4(K+1)(1-S)-Kh^2+4(K+1)(N-1)(1-S)e^2\right]}}{K(N-1)h^2+4(K+1)(1-S)+4(K+1)(N-1)(1-S)e^2}\right]$$

$$\text{(IX)}\quad \sigma_{b_{G_s(\overline{O_N-D_N})}} = \left[\frac{1}{\sqrt{N_s - 1}}\right] \cdot \left[\frac{\sqrt{4Nh^2\left[8-5h^2+4(N-1)(e^2+w) - 8U - 8(N-1)V\right]}}{8 + (N-5)h^2+4(N-1)(e^2 + w) - 8U - 8(N-1)V}\right]$$

$$\text{(X)}\quad \sigma_{b_{G_s\overline{O}_N}} = \left[\frac{1}{\sqrt{N_s - 1}}\right] \cdot \left[\frac{\sqrt{4Nh^2\left[4 - h^2 + 4(N-1)e^2\right]}}{4 + (N-1)h^2 + 4(N-1)e^2}\right]$$

The N_s refers to the number of sires tested while all other symbols were explained in connection with the coefficients of correlation and regression. Shown in Tables 4, 7, and 8 are numerical values of the second factors of each of the above standard errors of the coefficients of regression; the factor $\left[\frac{1}{\sqrt{N_s - 1}}\right]$ was not included. As N_s varies from 10 to 200, the factor $\left[\frac{1}{\sqrt{N_s - 1}}\right]$ varies from 1.333 to .0709.

Perhaps a more meaningful approach to the problem is to derive the standard error for the top five sires on a basis of the daughter-stablemate comparison. The expected variance of the breeding values of sires with a given index value is

$$\text{(XI)} \quad \sigma^2_{\hat{\bar{G}}_s} = \frac{h^2\sigma_p^2}{N_s}\left(1 - r^2_{G_sI}\right) + (I - \bar{I})^2\,\sigma^2_{b_{G_sI}}$$

$$\text{(XII)} \quad (I-\bar{I}) = z/b\ \sigma_I = z/b\ \sigma_p\sqrt{\frac{K(N-1)h^2 + 4(K+1)(1-S)+4(K+1)(N-1)(1-S)e^2}{4KN}}$$

Substituting the algebraic values of $r^2_{G_sI}$, z/b, σ_I and $\sigma^2_{b_{G_sI}}$ in the above formula for $\sigma^2_{\hat{\bar{G}}_s}$ it can be shown that the variance of a group of sires with a given index value is:

$$\text{(XIII)} \quad \sigma^2_{\hat{\bar{G}}_s} = h^2\,\sigma_p^2\left[\frac{4(K+1)(1-S)-Kh^2 + 4(K+1)(1-S)e^2}{K(N-1)h^2 + 4(K+1)(1-S)+4(K+1)(N-1)(1-S)e^2}\right]$$

$$\cdot\left[\frac{1}{N_s} + z/b\left(\frac{1}{N_s - 1}\right)\right]$$

In the above expression $\underline{N}_s$ represents the number of sires tested, σ^2_p the phenotypic variance of the trait involved and z/b the selection differential in terms of standard deviation units as shown in Table 9. All other symbols were defined previously.

Assume now that 1,000 daughters can be used for testing young sires and that the daughter-stablemate comparison is the index chosen for evaluating the sires. Shown in line 10 of Table 9 are standard errors for the average of the top five sires resulting from various systems of testing. In deriving the figures in Table 9 it was assumed that $\underline{h}^2 = .20$, $\underline{K} = 10$, $\underline{S} = .30$, and $\underline{e}^2 = 0$ and $\sigma_p = 80$.

In line 11 of Table 9 it is seen from the "t" values that in terms of their standard errors the expected genetic superiority of the 5 selected bulls varies only slightly when from 20 to 200 young sires are tested. Thus when 20 to 40 young sires are tested, the reliability of the expected genetic superiority of the top 5 is adequate.

The Natural Proof

The primary thing that limits the usefulness of the natural proof is the fact that the daughters are in one herd, thus giving rise to a relatively large environmental correlation between the daughters of a sire. If e^2 is .30 and h^2 = .20, formulas III and IV reach a maximum of .378 and .286 as N becomes infinitely large. In addition to this the standard error of the predicted breeding value is large. The above conditions are analagous to using the average of a sire's daughters, all of which are in one herd, to predict the breeding value of the sire for use in other herds. In measuring the accuracy and usefulness of natural proofs one should state where the sire is to be used. If the sire is to be used in the same herd in which he was tested, the proof can be quite accurate. On the other hand, if the sire is to be used in other herds or in AI, the proof is seriously wanting in accuracy.

If a proof based on daughters in a single herd is to be more accurate in predicting a sire for use in AI there must be some means of circumventing the environmental correlation between the daughters of the sire. It appears that such an index must include stablemates. If it is assumed that there is no correlation between herds and the breeding values of the sires used by the herds, that mating within herds is random, that the correlation between stablemates is S, that the correlation between the daughters of the sire is $h^2/4 + S$) and that the correlation between the daughters and stablemates is S, the correlation between the breeding value of the sire and the average of N daughters minus K stablemates in the same herd is:

$$\text{(XIV)} \quad r_{G_s}(\overline{O}_N - \overline{C}_K) = \sqrt{\frac{NKh^2}{K(N-1)h^2 + 4(K+N)(1-S)}} \; .$$

From the "b" values [illegible]
[illegible]ected genetic superiority of the 5
[illegible]ity when from 20 to 200 young sires are
[illegible] young sires are tested, the reliability of
[illegible]ority of the top 5 is adequate).

The [illegible] stating that limits the usefulness of the statistical proof is the fact that [illegible] daughters are in one herd, thus giving rise to a relatively [illegible] environmental correlation between the daughters of a sire. If r_s^2 is .70 and h^2 = .20, formulas III and IV reach a maximum of .378 and .206 as N becomes infinitely large. In addition to this the standard error of the predicted breeding value is large. The above conditions are analogous to using the average of a sire's dam sires, all of which are in one herd, to predict the breeding value of the sire for use in other herds. In research, the accuracy and usefulness of natural proofs one should state where the sire is to be used. If the sire is to be used in the same herd in which he was tested, the proof can be quite accurate. On the other hand, if the sire is to be used in other herds or in AI, the proof is seriously wanting in accuracy.

If a proof based on daughters in a single herd is [illegible] more accurate in predicting a sire's ROP use in AI there must be some means of eliminating the environmental correlation between the daughters of the sire. It appears that much on index must include stabilizers. If it is assumed that there is no correlation between herds and the breeding values of the sires used by the herds, that mating within herds is random, then the correlation between stabilizers is $\underline{S}$, that the correlation between the daughters of the sire is $h^2/(h^2 + S)$ and that the correlation between the daughters and stabilizers is $\underline{S}$, the correlation between the breeding value of the sire and the average of $\underline{K}$ daughters minus $\underline{K}$ stabilizers in the same herd is:

$$r_{\bar{a}} = \frac{\quad}{\sqrt{\quad^2 + h/(K+S)(1-S)}}$$

The regression of the breeding value of the sire on the same daughter - stablemate difference is

$$\text{(XV)}\quad b_{G_s(\overline{O}_N - \overline{C}_K)} = \frac{2NKh^2}{K(N-1)h^2 + 4(K+N)\ (1-S)} .$$

In deriving the above formulas it was assumed that the correlation between the daughters of a sire exceeded the correlation between stablemates by the quantity $h^2/4$. If the daughters as a group received special treatment, were selected, or were by a selected group of dams the correlation between daughters would be increased by an amount $\underline{e}^2$ and a term $4KNe^2$ should be added to the denominators of formulas XIV and XV. The accuracy of the single herd, daughter-stablemate index would be drastically reduced by only a small value for $\underline{e}^2$ and the maximum value of formulas XIV and XV would be low. For the proof in one herd to be of practical use to an AI stud the herd involved must have a large herd, all daughters and stablemates must be treated alike, both stablemates and daughters must be a random sample of their respective populations, and the sire in question must have been mated to a random sample of the herd. The validity of the single herd proof ishighly dependent on the integrity of the dairyman in whose herd it was made.

If the daughters were in the same herd but calved in different herd-year-seasons, the appropriate index would be a correct weighting of the daughter-stablemate differences for the several herd-year-seasons.

Shown in Table 10 are the correlations between the breeding value of a sire and the difference between the averages of $\underline{N}$ daughters and $\underline{K}$ stablemates in the same herd. Formula XIV was used to derive the values. It is apparent that a daughter-stablemate comparison based on cows in a single herd can be quite accurate in predicting the breeding values of sires, but it is essential that the correlation between the daughters of the sire (t) exceed the correlation between stablemates (S) by only the amount $h^2/4$ and that the correlation between daughters and stablemates be $\underline{S}$.

For the prior assumptions and with a given number of cows in the herd the most accurate proof results when the cows are evenly divided. For example when there are 40 daughters and 40 stablemates the correlation is greater than it is in the case where there are 50 daughters and 30 stablemates or 30 daughters and 50 stablemates.

[illegible]

Shown in Table 11 are the regression coefficients of the breeding value of a sire on the difference between the averages of N daughters and K stablemates in the same herd. The values in Tables 10 and 11 indicate that a proof in one herd can be quite accurate in predicting the breeding value of a sire.

In cases where the sires are mated to a selected group of cows, a combination of the daughter-stablemate difference and the daughter-dam difference would result in more accuracy; however in all progeny tests involving only one herd the factor that really limits the accuracy of the test is the amount by which the correlation between the daughters of a sire exceeds the correlation between stablemates of the daughters.

Discussion

To increase the genetic superiority of the tested young sires brought into the stud most artificial breeding organizations should be producing and testing more young sires and culling more. The test should be a daughter-stablemate comparison based on from 20 to 40 daughters per sire with each daughter having at least five stablemates. The greatest accuracy of the daughter-stablemate comparison is achieved when each sire tested has only one daughter per herd-year-season group and no two sires tested have daughters in the same herd-year-season group. When a sire has more than one daughter per herd-year-season group the accuracy of the daughter-stablemate comparison is probably more closely related to the number of different herd-year-season groups than to the number of daughters. Each AI organization should test from 4 to 8 young sires for each one it plans to add to the stud.

It is my opinion that all test matings should be made to a random sample of open heifers in progeny testing the young sires. This would probably avoid most of the preferential and non-random differences that can become confounded with the matings of young unproven sires. Further, by mating to open heifers, the mates of the young sires would probably be a more adequate sample of the genetic merit of the bulls currently in the AI stud. A breeding organization could test mate two groups of young sires each year but in each case all test matings should be made in a period of 3 to 4 weeks. Further, the date of the test matings should be timed so that it will jibe with the dates of publishing the DHIA sire summaries and the sire summary will be published soon after it is completed. Once the test data are available the bull studs should be objective and firm in culling the young sires on a basis of the test.

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It is recommended that all test matings should be made to a random
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young sires on a basis of the test.

The big objection to testing a large number of young sires is economic. At present the costs of producing, purchasing, testing and keeping young sires is exorbitant. It would seem that AI organizations could greatly reduce these costs by working out cooperative agreements with their clientele. It must be possible to purchase all young untested bulls for a nominal amount with additional payments to be made on a basis of the amount the daughter-stablemate comparison exceeds a specified level. Further, there must be ways of reducing the costs of testing and keeping young sires. In my opinion one of our greatest contributions as animal breeders would be to help AI organizations devise and put into operation plans whereby large numbers of young sires could be tested at low costs.

If AI organizations institute programs of routinely producing, purchasing and testing young sires whereby all test matings are made in a short period of time there seems little need for extensive use of incomplete records in proving sires. If a sire produces a considerable number of daughters failing to complete records there may be need to use a table of z/b values to regress the mean of those daughters completing records back toward the mean. It is probable that the completed records are from a selected group of cows. It would appear to be a sound policy to record for each sire being tested the fraction of daughters calving which complete records and adjust each sire's index accordingly.

At present most all sire indices are based on pounds of milk or fat per lactation and genetic gain is measured in this way. It seems that a more realistic measure would include the weights of the daughters and income over feed costs. By using a daughter-stablemate comparison, management differences between herds would be largely eliminated from income over feed costs. It is my opinion that yield per lactation gives an unfair advantage to the sire producing daughters larger than average; however, my knowledge is not sufficient to suggest a clearly superior alternative measure of production. A superficial analysis of the problem suggests that using the monetary value of the milk produced per lactation is better than the lactation yield of milk or fat. The monetary value of milk is subject to economic fluctuations, but the weightings of pounds of milk and fat in setting the monetary value change very little with time. Thus the monetary value could be adjusted for economic fluctuations and age of cow. Eventually we must measure production as net profit or in terms of efficiency; it is my opinion that yield per lactation is not sufficient.

Conclusions

To further increase the genetic superiority of the tested young sires brought into the stud, most AI studs should be routinely producing and testing more young sires on a basis of from 20 to 40 daughters per sire and culling from 3/4 to 7/8 of the young sires tested. AI studs should work out plans with their clientele whereby the stud can produce, purchase, house and test many young bulls economically.

Table 1. The expected correlations between the breeding value of a sire and the average of the N differences between the single records of each of his N daughters and the average of the K stablemates of each daughter using a heritability of .20.

N	e^2 = 0 and S = .25				e^2 = 0 and S = .30				e^2 = .02 and S = .25				e^2 = .02 and S = .30			
	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15
5	.38	.48	.49	.50	.39	.49	.51	.51	.37	.46	.48	.48	.38	.47	.49	.50
10	.51	.61	.63	.63	.52	.62	.64	.65	.47	.57	.59	.60	.49	.59	.61	.61
15	.58	.68	.70	.71	.60	.70	.71	.72	.53	.64	.65	.66	.55	.65	.67	.67
20	.64	.73	.75	.76	.65	.75	.76	.77	.57	.67	.69	.70	.59	.69	.70	.71
25	.68	.77	.79	.79	.69	.78	.80	.80	.60	.70	.72	.72	.62	.71	.73	.74
30	.71	.80	.81	.82	.73	.81	.82	.83	.63	.72	.74	.74	.64	.73	.75	.75
40	.76	.84	.95	.85	.77	.85	.86	.86	.66	.75	.76	.77	.67	.76	.78	.78
50	.80	.86	.87	.88	.81	.87	.88	.88	.68	.77	.78	.79	.69	.78	.79	.80
60	.82	.88	.89	.89	.83	.89	.90	.90	.69	.78	.79	.80	.71	.79	.80	.81
70	.84	.90	.90	.91	.85	.90	.91	.91	.71	.79	.80	.81	.72	.80	.81	.82
80	.86	.91	.91	.92	.86	.91	.92	.92	.71	.80	.81	.82	.73	.81	.82	.82
90	.87	.92	.92	.93	.88	.92	.93	.93	.72	.80	.82	.82	.73	.81	.83	.83
100	.88	.92	.93	.93	.89	.93	.93	.94	.73	.81	.82	.83	.74	.82	.83	.83
200	.93	.96	.96	.96	.94	.96	.97	.97	.76	.83	.84	.85	.77	.84	.85	.85

Table 2. The expected correlations between the breeding value of a sire and the average of the N differences between the single records of each of his N daughters and the averages of each daughter's K stablemates, using a heritability of .25.

N	e^2 = 0 and S = .25				e^2 = 0 and S = .30				e^2 = .02 and S = .25				e^2 = .02 and S = .30			
	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15	K=1	K=5	K=10	K=15
5	.42	.52	.54	.55	.43	.53	.55	.56	.41	.51	.52	.53	.42	.52	.54	.54
10	.55	.65	.67	.68	.56	.67	.68	.69	.52	.62	.64	.64	.53	.63	.65	.66
15	.63	.73	.74	.75	.64	.74	.75	.76	.58	.68	.70	.70	.59	.69	.71	.72
20	.68	.77	.79	.79	.69	.78	.80	.80	.62	.72	.73	.74	.63	.73	.74	.75
25	.72	.81	.82	.82	.73	.82	.83	.83	.65	.74	.76	.76	.66	.75	.77	.77
30	.75	.83	.84	.85	.76	.84	.85	.86	.67	.76	.78	.78	.68	.77	.79	.79
40	.80	.87	.87	.88	.81	.87	.88	.89	.70	.79	.80	.80	.71	.80	.81	.81
50	.83	.89	.90	.90	.84	.89	.90	.91	.72	.80	.82	.82	.73	.81	.82	.83
60	.85	.90	.91	.91	.86	.91	.92	.92	.73	.81	.83	.83	.75	.82	.84	.84
70	.87	.92	.92	.92	.87	.92	.93	.93	.74	.82	.83	.84	.76	.83	.84	.85
80	.88	.93	.93	.93	.89	.93	.94	.94	.75	.83	.84	.84	.76	.84	.85	.85
90	.89	.93	.94	.94	.90	.94	.94	.94	.76	.83	.85	.85	.77	.84	.85	.86
100	.90	.94	.94	.95	.91	.94	.95	.95	.77	.84	.85	.85	.78	.85	.86	.86
200	.93	.97	.97	.97	.95	.97	.97	.97	.79	.86	.87	.87	.80	.87	.88	.88

Table 3. The regression of the breeding value of a sire on the average of the N differences between his N daughters and the average of each daughter's K stablemates.

N	h^2 = .20								h^2 = .25							
	e^2=0 & S=.25		e^2=0 & S=.30		e^2=.02&S=.25		e^2=.02&S=.30		e^2=0 &S=.25		e^2=0 &S=.30		e^2=.02&S=.25		e^2=.02&S=.30	
	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15
5	.49	.50	.52	.53	.46	.47	.48	.50	.58	.59	.61	.62	.55	.56	.58	.59
10	.78	.80	.82	.84	.70	.72	.74	.75	.90	.92	.94	.95	.81	.83	.85	.87
15	.98	1.00	1.02	1.04	.85	.87	.89	.91	1.10	1.12	1.14	1.16	.97	.99	1.01	1.02
20	1.13	1.14	1.16	1.18	.96	.97	.99	1.01	1.24	1.26	1.28	1.29	1.07	1.09	1.11	1.13
25	1.23	1.25	1.27	1.28	1.03	1.05	1.07	1.08	1.34	1.36	1.38	1.39	1.15	1.16	1.18	1.20
30	1.32	1.33	1.35	1.37	1.09	1.11	1.12	1.14	1.42	1.43	1.45	1.46	1.20	1.22	1.24	1.25
40	1.44	1.45	1.47	1.48	1.17	1.19	1.20	1.22	1.53	1.54	1.56	1.57	1.28	1.29	1.31	1.33
50	1.53	1.54	1.55	1.56	1.22	1.24	1.26	1.27	1.61	1.62	1.63	1.64	1.33	1.34	1.36	1.38
60	1.59	1.60	1.61	1.62	1.26	1.28	1.30	1.31	1.66	1.67	1.68	1.69	1.37	1.38	1.40	1.41
70	1.64	1.65	1.66	1.67	1.29	1.31	1.32	1.34	1.70	1.71	1.72	1.73	1.39	1.41	1.42	1.44
80	1.67	1.68	1.69	1.70	1.32	1.33	1.35	1.36	1.73	1.74	1.75	1.76	1.41	1.43	1.44	1.46
90	1.71	1.71	1.72	1.73	1.33	1.35	1.37	1.38	1.76	1.77	1.78	1.78	1.43	1.44	1.46	1.47
100	1.73	1.74	1.75	1.75	1.35	1.36	1.38	1.39	1.78	1.79	1.80	1.80	1.45	1.46	1.47	1.49
200	1.86	1.86	1.87	1.87	1.42	1.43	1.45	1.46	1.88	1.89	1.89	1.90	1.51	1.52	1.54	1.55

Table 4. The standard errors of the regression of the breeding value of a sire on the average of N differences between his N daughters and the average of each daughter's K stablemates.

N	h^2 = .20								h^2 = .25							
	e^2=0 &S=.25		e^2=0 &S=.30		e^2=.02&S=.25		e^2=.02&S=.30		e^2=0 &S=.25		e^2=0 &S=.30		e^2=.02&S=.25		e^2=.02&S=.30	
	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15
5	.86	.86	.87	.88	.84	.85	.85	.86	.91	.91	.92	.93	.89	.90	.91	.91
10	.98	.98	.98	.99	.95	.96	.96	.97	.99	1.00	1.00	1.00	.98	.98	.99	.99
15	.99	1.00	.99	1.00	.99	.99	.99	1.00	.99	.99	.99	.99	1.00	1.00	1.00	1.00
20	.99	.99	.99	.98	1.00	1.00	1.00	1.00	.97	.97	.96	.96	1.00	1.00	.99	.99
25	.97	.97	.96	.96	1.00	1.00	1.00	1.00	.94	.93	.93	.92	.99	.99	.98	.98
30	.95	.94	.94	.93	1.00	.99	.99	.99	.91	.90	.89	.88	.98	.98	.97	.97
40	.90	.89	.88	.87	.98	.98	.98	.98	.85	.84	.83	.82	.96	.96	.95	.94
50	.85	.84	.83	.83	.97	.97	.97	.96	.79	.79	.78	.77	.94	.94	.93	.93
60	.81	.80	.79	.78	.96	.96	.95	.95	.75	.74	.73	.72	.93	.92	.92	.91
70	.77	.76	.75	.74	.96	.95	.95	.94	.71	.70	.69	.68	.92	.91	.91	.90
80	.74	.73	.72	.71	.95	.94	.94	.93	.68	.67	.66	.65	.91	.90	.90	.89
90	.71	.70	.69	.68	.94	.94	.93	.92	.65	.64	.63	.62	.90	.90	.89	.88
100	.68	.67	.66	.65	.94	.93	.92	.92	.62	.61	.60	.60	.89	.89	.88	.87
200	.52	.51	.50	.49	.91	.90	.89	.89	.47	.46	.45	.44	.86	.85	.84	.84

Table 5. The "t" values calculated by the ratio $b_{G_s}\ \overline{(0-\overline{C})}/\sigma_b$

N	e^2=0 & S=.25		e^2=0 & S=.30		e^2=.02&S=.25		e^2=.02&S=.30		e^2=0&S=.25		e^2=0&S=.30		e^2=.02&S=.25		e^2=.02&S=.30	
	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15	K=10	K=15
5	.57	.58	.59	.60	.54	.55	.57	.57	.64	.65	.66	.68	.61	.62	.64	.65
10	.80	.82	.83	.85	.74	.75	.76	.78	.90	.92	.94	.96	.83	.84	.86	.87
15	.98	1.00	1.02	1.04	.86	.88	.89	.91	1.11	1.13	1.15	1.17	.97	.99	1.01	1.02
20	1.14	1.15	1.18	1.20	.96	.97	.99	1.01	1.28	1.30	1.33	1.35	1.08	1.09	1.12	1.14
25	1.27	1.29	1.32	1.34	1.03	1.05	1.07	1.09	1.43	1.46	1.49	1.51	1.16	1.18	1.20	1.22
30	1.39	1.41	1.44	1.47	1.09	1.11	1.13	1.15	1.57	1.59	1.63	1.66	1.23	1.25	1.27	1.30
40	1.61	1.63	1.67	1.69	1.19	1.21	1.23	1.25	1.81	1.84	1.88	1.91	1.33	1.35	1.38	1.40
50	1.80	1.83	1.86	1.89	1.26	1.28	1.30	1.32	2.02	2.06	2.10	2.14	1.41	1.43	1.46	1.49
60	1.97	2.00	2.04	2.07	1.31	1.33	1.36	1.38	2.22	2.25	2.30	2.34	1.47	1.49	1.52	1.55
70	2.12	2.16	2.20	2.24	1.35	1.37	1.40	1.42	2.39	2.44	2.49	2.53	1.52	1.54	1.57	1.60
80	2.27	2.31	2.36	2.40	1.39	1.41	1.44	1.46	2.56	2.60	2.66	2.70	1.56	1.58	1.61	1.64
90	2.41	2.45	2.50	2.54	1.42	1.44	1.47	1.49	2.72	2.76	2.82	2.87	1.59	1.61	1.64	1.67
100	2.54	2.58	2.63	2.68	1.44	1.46	1.49	1.52	2.86	2.91	2.97	3.02	1.61	1.64	1.67	1.70
200	3.59	3.65	3.73	3.79	1.57	1.59	1.63	1.65	4.05	4.12	4.20	4.27	1.76	1.78	1.82	1.85

Table 6. The correlation between the breeding value of a sire (G_s) and the average difference between N of his daughters and their respective dams ($\overline{O}_N - \overline{D}_N$) and the regressions of G_s on ($\overline{O}_N - \overline{D}_N$)*.

N	Correlations								Regressions							
	$h^2 = .20$				$h^2 = .25$				$h^2 = .20$				$h^2 = .25$			
	U = .25		U = .30		U = .25		U = .30		U = .25		U = .30		U = .25		U = .30	
	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$
5	.41	.40	.42	.41	.46	.44	.47	.50	.33	.32	.36	.34	.42	.40	.45	.42
10	.53	.51	.55	.52	.59	.56	.60	.57	.57	.52	.61	.55	.69	.63	.73	.66
15	.61	.57	.63	.58	.66	.62	.68	.64	.75	.66	.79	.69	.88	.78	.93	.81
20	.67	.62	.68	.63	.72	.67	.73	.68	.89	.76	.93	.79	1.02	.89	1.07	.92
25	.71	.65	.72	.66	.75	.70	.77	.71	1.00	.84	1.04	.87	1.14	.97	1.18	1.00
30	.74	.67	.75	.68	.78	.72	.79	.73	1.09	.90	1.13	.93	1.22	1.03	1.27	1.06
40	.78	.70	.80	.71	.82	.75	.83	.76	1.23	.99	1.27	1.02	1.36	1.12	1.39	1.14
50	.82	.73	.83	.73	.85	.77	.86	.78	1.33	1.06	1.37	1.08	1.45	1.18	1.48	1.20
60	.84	.74	.85	.75	.87	.78	.88	.79	1.41	1.11	1.45	1.13	1.52	1.23	1.55	1.25
70	.85	.76	.87	.76	.89	.79	.89	.80	1.47	1.14	1.50	1.16	1.57	1.26	1.60	1.28
80	.87	.76	.88	.77	.90	.80	.91	.81	1.52	1.17	1.55	1.19	1.62	1.29	1.64	1.30
90	.88	.77	.89	.78	.91	.81	.91	.81	1.56	1.19	1.59	1.21	1.65	1.31	1.68	1.32
100	.86	.78	.90	.78	.92	.81	.92	.82	1.60	1.21	1.63	1.23	1.68	1.33	1.70	1.34
200	.92	.81	.95	.81	.96	.84	.96	.84	1.78	1.31	1.79	1.32	1.83	1.41	1.84	1.42

*It is assumed that w and V are zero.

Table 7. The standard errors of the regression of the breeding value of a sire on the average of N daughters minus their N dams, and the corresponding "t" ratios.*

N	Standard Errors								"t" Values							
	$h^2 = .20$				$h^2 = .25$				$h^2 = .20$				$h^2 = .25$			
	U = .25		U = .30		U = .25		U = .30		U = .25		U = .30		U = .25		U = .30	
	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$
5	.74	.73	.77	.75	.81	.80	.83	.82	.45	.43	.47	.45	.51	.50	.54	.52
10	.90	.88	.92	.89	.95	.93	.96	.94	.63	.59	.66	.61	.73	.68	.76	.70
15	.97	.94	.98	.95	.99	.97	1.00	.98	.77	.70	.81	.72	.89	.80	.93	.83
20	.99	.97	1.00	.98	1.00	.99	1.00	1.00	.89	.78	.93	.81	1.03	.89	1.07	.92
25	1.00	.99	1.00	.99	.99	1.00	.98	1.00	1.00	.85	1.04	.88	1.15	.97	1.20	1.00
30	1.00	.99	.99	1.00	.97	1.00	.96	1.00	1.09	.90	1.14	.93	1.26	1.03	1.31	1.06
40	.97	1.00	.96	1.00	.93	.99	.92	.99	1.26	.99	1.32	1.02	1.45	1.13	1.52	1.16
50	.94	1.00	.93	1.00	.89	.98	.87	.98	1.41	1.06	1.47	1.08	1.62	1.20	1.69	1.23
60	.91	.99	.89	.99	.85	.97	.83	.97	1.55	1.11	1.61	1.13	1.78	1.26	1.86	1.29
70	.88	.99	.86	.99	.82	.97	.80	.96	1.67	1.15	1.74	1.18	1.92	1.30	2.01	1.33
80	.85	.98	.83	.98	.79	.96	.83	.95	1.79	1.19	1.86	1.21	2.05	1.34	2.14	1.37
90	.82	.98	.80	.98	.76	.95	.80	.95	1.90	1.22	1.98	1.24	2.18	1.38	2.27	1.40
100	.80	.98	.78	.97	.73	.94	.78	.94	2.00	1.24	2.08	1.26	2.29	1.40	2.40	1.43
200	.63	.95	.61	.95	.56	.91	.61	.91	2.83	1.38	2.95	1.40	3.24	1.55	3.39	1.57

*It is assumed that w and V are zero.

Table 8. The correlations, regressions, standard errors of regression and "t" values associated with the relationship between the daughter averages and the breeding value of the sire.

	Correlations				Regressions				Standard Error of Regression				"t" Values			
	$h^2 = .20$		$h^2 = .25$		$h^2 = .20$		$h^2 = .25$		$h^2 = .20$		$h^2 = .25$		$h^2 = .20$		$h^2 = .25$	
N	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$	$e^2=0$	$e^2=.02$
5	.46	.44	.50	.48	.42	.39	.50	.47	.81	.79	.87	.85	.51	.49	.58	.55
10	.59	.55	.63	.60	.69	.61	.80	.72	.95	.92	.98	.96	.73	.66	.82	.75
15	.66	.62	.71	.66	.88	.76	1.00	.87	.99	.97	1.00	.99	.89	.78	1.00	.88
20	.72	.65	.76	.70	1.03	.86	1.14	.97	1.00	.99	.99	1.00	1.03	.87	1.15	.97
25	.75	.68	.79	.72	1.14	.93	1.25	1.05	.99	1.00	.97	1.00	1.15	.93	1.29	1.05
30	.78	.70	.82	.74	1.22	.99	1.33	1.10	.97	1.00	.94	.99	1.26	.99	1.41	1.11
40	.82	.73	.85	.77	1.36	1.07	1.45	1.19	.93	1.00	.89	.98	1.45	1.07	1.63	1.21
50	.85	.75	.88	.79	1.45	1.13	1.54	1.24	.89	.99	.84	.97	1.62	1.14	1.83	1.28
60	.87	.76	.89	.80	1.52	1.17	1.60	1.28	.85	.99	.80	.96	1.78	1.19	2.00	1.33
70	.89	.77	.91	.81	1.57	1.20	1.65	1.31	.82	.98	.76	.95	1.92	1.23	2.16	1.37
80	.90	.78	.92	.82	1.62	1.22	1.68	1.33	.79	.97	.73	.94	2.05	1.26	2.31	1.41
90	.91	.79	.92	.82	1.65	1.24	1.71	1.35	.76	.97	.70	.94	2.18	1.28	2.45	1.44
100	.92	.79	.93	.83	1.68	1.26	1.74	1.36	.73	.96	.67	.93	2.29	1.31	2.58	1.46
200	.96	.82	.96	.85	1.83	1.34	1.86	1.43	.56	.94	.51	.90	3.24	1.42	3.65	1.59

Table 9. The standard errors of the top 5 sires for tests based on a total of 1,000 daughters.

Variable	Number of Sires Tested (N_s)						
	10	20	25	40	50	100	200
z/b	0.74	1.21	1.34	1.59	1.70	2.06	2.34
$(I-\bar{I})=z/b\sigma_I$	13.3	21.8	24.2	28.8	30.8	37.8	44.1
$b_{G_sI}(I-\bar{I})$	23.3	33.8	35.6	36.6	35.7	31.0	22.9
$(1-r^2_{G_sI})$	.135	.226	.260	.360	.422	.590	.740
$\frac{1}{N_s}$	.100	.050	.040	.025	.020	.010	.005
$(I-\bar{I})^2$	176	474	583	827	950	1432	1941
$\frac{1}{N_s - 1}$	.1111	.0526	.0417	.0256	.0204	.0101	.0050
$(N_s-1)\sigma^2_{b_{G_sI}}$	.436	.689	.774	.922	.980	.960	.787
$\sigma^2_{\hat{G}_s}$	25.8	31.6	32.1	31.1	29.8	21.4	12.1
$\sigma_{\hat{G}_s}$	5.1	5.6	5.7	5.6	5.5	4.6	3.5
"t"	4.57	6.04	6.25	6.52	6.53	6.70	6.58

$\sigma_p = 80$ and $h^2\sigma^2 = 1{,}280$.

$h^2 = .20$, $S = .30$, $e^2 = 0$, $K = 10$

$$\sigma_I = \sigma_p \sqrt{\frac{K(N-1)h^2 + 4(K+1)(1-S) + 4(K+1)(N-1)(1-S)e^2}{4KN}}$$

$$\text{"t"} = \frac{b_{G_sI}\,(I-\bar{I})}{\sigma_{\hat{G}_s}}$$

Table 10. The correlations between the breeding value of a sire and the difference between the average of N daughters and K stablemates in the same herd.

$$(h^2 = .20,\ S = .30,\ \text{and}\ t = \frac{h^2}{4} + S.)$$

N	K							
	5	10	15	20	30	40	50	∞
10	.443	.520	.556	.577	.601	.614	.622	.659
20	.474	.572	.622	.652	.687	.707	.720	.778
30	.486	.594	.650	.685	.725	.749	.764	.835
40	.492	.606	.666	.702	.747	.773	.789	.869
50	.496	.613	.675	.714	.761	.788	.806	.891
∞	.513	.646	.719	.767	.825	.861	.884	1.000

Table 11. The regression of the breeding value of a sire on the difference between the averages of N daughters and K stablemates in the same herd.

$$(h^2 = .20,\ S = .30 \text{ and } t = \frac{h^2}{4} + S)$$

N	K							
	5	10	15	20	30	40	50	∞
10	.392	.541	.619	.667	.723	.755	.775	.870
20	.449	.656	.774	.851	.945	1.000	1.036	1.212
30	.472	.706	.845	.938	1.053	1.121	1.167	1.395
40	.485	.734	.886	.988	1.116	1.194	1.246	1.509
50	.493	.752	.912	1.020	1.158	1.242	1.299	1.587
∞	.526	.834	1.034	1.176	1.364	1.482	1.562	2.000

N = 100 K= 100.

$b_{G_s}(\overline{O}_N - \overline{C}_K) = 1.575.$

DISCUSSION

DR. DICKINSON: Could we carry this a little further? After the bulls are suitably proven, could the USDA just discontinue to summarize them after they have a hundred or two hundred daughters? This would cut down on the amount of work.

DR. TOUCHBERRY: I think that this would be a sound practice except in the case of an extremely old bull that was to be compared with the young bulls.

DR. CARTER: If you did that, would you carry all daughters then, or just pick up a new crop of daughters to evaluate?

DR. TOUCHBERRY: I would favor picking up a new crop. The new group of daughters would be more representative of the current genetic merit of the herds of the clientele.

DR. BARR: Then accuracy for the proof is, as you say, relatively unimportant?

DR. TOUCHBERRY: I didn't say it was unimportant. I said ---

DR. BARR: Relative to the selection intensity.

DR. TOUCHBERRY: After obtaining a certain number of daughters, the change in accuracy is relatively unimportant, as compared to the reduction in selection intensity that can be practiced if a large number per sire is used.

DR. BARR: Well, to continue, can we make enough progress by selecting on pedigrees to not worry about sampling?

DR. TOUCHBERRY: I would doubt this. I think that you gave some figures a moment ago on the use of the pedigree. All of the young bulls to be tested should be chosen on the basis of their pedigree, and the gain resulting from progeny testing would be in addition to that, would it not?

DR. BARR: Oh, well, certainly; this is the logical way to do it. But could you do this? -- You are talking about a fairly substantial number in a sampling program.

DR. TOUCHBERRY: Yes.

DR. BARR: Fifty to sixty.

DR. TOUCHBERRY: And a relatively small population.

DISCUSSION

Could we carry this a little further? After the bulls proven, could the dual purpose discontinue to manufacture them after number or two hundred [illegible]? This would cut down on the [illegible]

[illegible]: I think that this would be sound practice [illegible] of an extremely old bull that was to be compared [illegible] bulls.

[illegible] you did that, what you carry all daughters then, [illegible] crop of daughters to evaluate?

DR. TOUR [illegible]: I would favor picking up a new crop. The new group of daughters would be more re[illegible] of the [illegible] genetic [illegible] of the herds of [illegible] clientele.

DR. [illegible] accuracy, [illegible] process [illegible] as you say, [illegible]

TOUCHBERRY: I didn't say it was quite urgent. I said ---

[illegible]: Relative to the selection intensity.

DR. TOUCHBERRY: After obtaining a certain number of daughters, the change in accuracy is relatively unimportant, as compared to the reduction in selection intensity that can be [illegible] if a large number [illegible]

[illegible]: Well, to [illegible], can we wait enough [illegible] agree to not worry about sampling?

[illegible]: I would doubt this. I think that you have some [illegible] on the pedigree of the pedigree. All of the young bulls [illegible] be chosen on the basis of their pedigree, and the gain [illegible] of a proven bull would be in addition to that, would it not?

[illegible] certainly this is the logical way to do it.

-- You are talking [illegible]

DR. HENDERSON: It depends entirely upon the population size. As you go down to a small population--

DR. TOUCHBERRY: Yes, right.

DR. HENDERSON: And Dickerson showed this.

DR. BARR: Yes, but what is the size of the population to date?

DR. HENDERSON: Oh, let us say a two or three hundred cow herd. But this is a wild guess; I don't know.

DR. BARR: Well, what is it? I would like to know.

DR. HARVEY: He is way off!

DR. HENDERSON: In a thousand cow herd, you wouldn't, I guess?

DR. BARR: Well, I was speaking more of AI situations. And even for AI studs, I wouldn't consider sampling programs for some.

DR. HENDERSON: There is another factor now that enters in. Dale Van Vleck checked on costs per individual bull and even though I agree wholeheartedly with Dr. Touchberry in trying to sample more bulls and not worry about getting a large number of daughters per sire--but the optimum number to sample has changed from an economic standpoint.

DR. MEADOWS: I think, within reason, that we have to live with the single herd proof in at least a limited number of herds. If we could increase the number of young bulls sampled, even though the accuracy per bull isn't extremely high, we might be just as well off. There is such a thing as risk and gain, you know.

DR. TOUCHBERRY: Yes.

DR. MEADOWS: That bothers people who are involved. They are willing to take the risk, if they can obtain the gain. The question that I have--and I think that it was incorporated with our report, as a matter of fact, in Portland, Oregon, and they struck it out! It is that perhaps we should consider, at least, a limited number of herds, and go ahead and decrease the number sampled each year, provided they would let me help them create the bull, to begin with--his pedigree.

DR. TOUCHBERRY: You know, there were such schemes about fifty or sixty years ago--a Frenchman suggested such a crossing scheme for testing bulls and herds, and in talking about four or five herds, I believe that one could work out a good proof of four or five sires on four or five herds. In each herd there should be an equal number of randomly chosen cows mated to each sire, and the management should not favor one sire's daughters over another.

MR. [illegible]: In a general sense, yes, in population size, [illegible] well [illegible].

MONTGOMERY: Yes, sir.

MR. HENDERSON: Are [illegible] shown that.

MR. [illegible] Yes, but what is the size of the population to [illegible]

[illegible] Oh, let us [illegible] two or three hundred [illegible] with [illegible] I don't know.

MR. [illegible]: Well, what is it? I would like to know.

MR. MONTGOMERY: He is way off!

MR. [illegible]: In a thousand cow herd, you wouldn't [illegible].

MR. [illegible]: Well, I was speaking more of AI situations, and even [illegible] wouldn't consider supplying pregnant [illegible].

[illegible] There is another factor now that enters in. [illegible] individual but [illegible] even though I agree wholeheartedly [illegible] trying to supply more bulls and not worry about [illegible] of daughters per sire--but the optimum number to [illegible] from an economic standpoint.

[illegible] bulls, which reason, that we have to live with the [illegible] at least a limited number of herds. If we could increase [illegible] supplied, even though the accuracy per bull isn't [illegible] be just as well off. There is such a thing as [illegible]

[illegible] bulls people who are involved. They are willing [illegible] to obtain the yield. The question that [illegible] with our report, as a matter of fact, [illegible] I don't. It is time perhaps we should [illegible] back, and go around and reconsider [illegible] they would let us help them create

DR. MEADOWS: Well, I am sure that I could choose among those four bulls, but then if another group sampled four, the accuracy of choosing among those---

DR. TOUCHBERRY: It wouldn't be so good.

DR. MEADOWS: But it still wouldn't offset all of this, because we have sampled only four herds and in comparing these bulls with another group of four, herd differences could exist to a considerable extent.

DR. GAUNT: Another possibility is when you discover how superior these sires are, how good they are, kill these sires after having built up a semen bank. And I believe that we can store semen more economically than we can keep bulls for five years.

DR. VAN VLECK: This may have some bearing on this--I asked the Eastern people how much it was costing them to sample one young bull--this is one bull purchased--until he is proved, and this was ten thousand dollars, of which only about five hundred dollars of that is original purchase price.

DR. LEGATES: Yes.

DR. VAN VLECK: So that makes quite a difference when you set up a sampling program, particularly for the breeds with small numbers.

DR. LEGATES: Yes, but now why would this cost so much?

DR. VAN VLECK: I was always figuring around $2,500, but they said about $10,000, and they actually have the figures. I don't know. And it might be cheaper at that rate.

DR. HENDERSON: Isn't there another approach?

DR. LEGATES: I don't know; I have talked to Mr. Baldwin, and we have done a little figuring, and we wouldn't worry about breeding such a high percentage of our cow population to what we call a proved bull, and bring them in and sample them, and save enough semen for use as the sires of other bulls, and get them out of our way--do you see what I mean? Then we can get almost as much progress, and economically we may actually be ahead, because we would just keep a bull, say, two and a half or three years, and get rid of him, and just save enough semen, and have that available for rebreeding sons by him if he is good enough, and if not, toss it out.

DR. HICKMAN: I think it depends entirely on what the selection differential is in determining the choice of proven bulls out of the group that have been tested. I have some results which indicate that if you have to use a higher selection intensity than thirty percent, you had better not.

DR. LEGATES: You mean, you had better not save sons?

DR. HICKMAN: Yes, like three out of ten or more, you are better off not to use proven bulls at all.

DR. LEGATES: There is some relationship, I think where it is either a lot less costly, and you will get just as much progress.

DR. VAN VLECK: The Eastern Holstein stud has six or seven hundred thousand cows in the breeding system. I think the selection there comes out, oh, about one in twenty, or one in twenty-five, and you can certainly spend $10,000 on a bull. They are still making more progress, and it includes from, I think, $2.50 per hundredweight of milk for feed cost for the improvement, and they are still better off sampling, say, four hundred bulls, even if they are going to return only five or ten of those per year to the stud, but this just falls into what you are saying, actually.

DR. MEADOWS: $10,000 for a bull.

DR. VAN VLECK: $10,000 for a bull.

DR. TOUCHBERRY: I don't see why it costs so much. After all some people produce and feed cattle to make money.

DR. VAN VLECK: Well, paying $2,500 for the young bull is not going to change it so much.

DR. TOUCHBERRY: No.

DR. VAN VLECK: Not for a large stud.

DR. HENDERSON: Well, I think that it is very clear that on a large population you make a choice of these through highly selected AI proven bulls. You sample a large number of bulls each time, and it is awfully hard to anybody to compete with this kind of a situation, I think. At this point, it would be extremely difficult for small organizations, or small herds. Or even large herds.

DR. MCGILLIARD: But aren't those curves so flat that it doesn't make much difference, that it doesn't matter much?

DR. HICKMAN: No, it isn't that flat.

DR. VAN VLECK: Holstein, five to ninety percent for proved bulls, four years or so, and for breeds with smaller numbers it drops down to about fifty or sixty percent, and changes a good bit, depending on population size. But you are right, it doesn't make much difference there.

DR. MCGILLIARD: The optimum changes.

DR. HENDERSON: Oh, yes.

DR. VAN VLECK: Right.

DR. HENDERSON: So that for the economics involved, you will, obviously, move to the left of the genetic optimum, in any situation, and it is pretty long on a herd, fortunately.

DR. TOUCHBERRY: Well, I think that if we want to have a greater rate of change we will have to produce and sample more young sires.

MR. RUMLER: What is the basis for suggesting a separate publication between the AI and the non-AI, so long as you indicate the number of daughters, and the number of herds in which those daughters are located? What is the significant difference? Because those are the variables that are important. AI and non-AI is inconsequential, isn't it, so long as you know the number of daughters and the number of different herds? Am I right? Or am I wrong in understanding it?

DR. TOUCHBERRY: So long as the number of daughters, the number of herds, and the number of daughters per herd is known and the correct weighting of the information is made there is no real difference between natural and AI proofs. However, when all daughters are in one herd, it is easy to bias the proof by giving the daughters special management.

DR. FREEMAN: Well, there is now, and maybe I should answer this, because I said that we are doing it, and the reason that we are doing it is primarily because of the reliability, the increased reliability of the proof with more information in it. So it is, essentially, setting the natural proofs aside and mentioning them in terms of reliability and accuracy, and when natural proofs are just intermingled down the list, they are not nearly so easy for the average farmer to distinguish.

DR. BURNSIDE: Certainly, in publications that are going to the breeder, there is something to be said for separating AI and natural proofs.

DR. FREEMAN: We may be wrong, but that is our thinking.

DR. CARTER: And even though we regress the natural proof, the standard deviation for predicting is larger than for AI proofs. And this is the thing that is hard to get across to the rank and file of dairymen; even though this proof of bulls will end up here, that on the individual bull your accuracy is quite different.

DR. TOUCHBERRY: The standard deviations of the regression of the breeding value of a sire on the average of N daughters in one herd was shown in one of the tables in the handout and these standard deviations were the largest of all the indices compared.

DR. MEADOWS: Doesn't this selection intensity that you have expressed here enter with almost every phase of selection?

DR. TOUCHBERRY: Yes.

DR. MEADOWS. Again, I have sort of argued all the way along that the USDA's work was particularly important to us in determining from which of the bulls that have been used do we want to sample sons.

DR. TOUCHBERRY: Yes.

DR. MEADOWS: This again is selection intensity, as I see it. I am not really worried so much about the bulls--about which bulls that I choose from initially, and I don't want to wait forever to decide whether I just want to use the bull. But I would really like this accuracy to come in when I am trying to decide which of the bulls that have been used should be the sires of the next generation of young bulls sampled.

DR. TOUCHBERRY: Yes.

DR. MEADOWS: And I think that is the real importance of this so-called accuracy that we have been talking about. And the same thing is true with the index of the cow that eventually becomes the dam of the young bull that I am going to choose; I would like for this to be as accurate as possible, because I would like to stick with a few of the best cows that I have.

DR. TOUCHBERRY: We would still have that accuracy if we continued to report the records. The progeny test of the young sires would be a screening test to throw out the young sires shown to be undesirable, but we would continue to get records on the progeny of the best young sires.

DR. MEADOWS: And my culling level is important in all three stages.

DR. TOUCHBERRY: Yes. Certainly, in a planned progeny testing program of young sires I agree that one should choose sons of outstanding bulls.

DR. MEADOWS: One of the difficult problems at the moment is deciding which bulls you are going to bank. You would like to have a bank of semen from bulls from which you want to sample sons, but you have to get this before you are completely certain, and this presents quite a problem.

DR. TOUCHBERRY: I think that you shouldn't be banking semen from these before you get the progeny test, and just plan on turning bulls over in as short a time as possible. After all, if a bull has been in a stud for, let us say, seven or eight years, the genetic trend in the population should begin to catch up with this bull.

DR. MEADOWS. Well, I am glad that you brought this out, because in the last four or five years, we haven't been concerned with anything but accuracy. We have forgotten everything else that enters into the animal improvement. And we ought to pay attention to some of these other factors.

DR. PLOWMAN: Were you suggesting that we should be evaluating bulls based on an input-output relationship, which would take into consideration size and so on? And if we did this, do you think we have enough adequate data in DHIA to do it? And if we did it, do you think this would change the rank of bulls as compared to what we are doing now?

DR. TOUCHBERRY: Well, I don't think that we could do it very well at the present on an input-output basis because of lack of data. I suppose it depends on what you mean by input-output.

DR. PLOWMAN: Well, I was thinking in terms of feed input-milk output relationships, which would take into consideration the things you mentioned--size, maintenance cost, and things like this.

DR. TOUCHBERRY: I don't know. I really don't know whether it would change things much or not, but I think that we should be considering costs and returns if we are going to keep on talking about

efficiency; perhaps using a simple thing such as the monetary value of the product produced would be an improvement. We are still talking about pounds of milk or pounds of fat and not the two combined.

DR. PLOWMAN: Yes, well, this is what I mean. We would combine our feed costs and so--in terms of input and value of the product that we get out, and evaluate both on this basis.

DR. TOUCHBERRY: I think, eventually, that we will have to come to some system like this.

DR. PLOWMAN: Do you think that we can collect this kind of data through DHIA to do it accurately enough?

DR. TOUCHBERRY: I don't know.

DR. MEADOWS: Our economists are playing with this, but the only trouble that I have with them is the fact that they don't want to use any mature equivalent factors when they convert into dollars. And I don't know how to combat this. I am afraid that all our two-year-olds are going to leave. We have been ranking our cows on milk, and they say this doesn't make any sense. They want to know profits and they convert it to dollars. Well, this is perfectly all right with me if they give the two-year-olds a chance when they convert to dollars, or else they are just going to have to consider the two-year-olds separately and assume that they made the right decisions on everything else. They are also trying to bring in the other factors that you were talking about, but I would say they haven't had much success at this as yet. But in fact, you know the gross return from the sales of milk and this makes a considerable difference.

DR. TOUCHBERRY: It does make a difference in some cases, yes.

DR. HARVEY: This adjustment in sire proofs which you mentioned for selection practiced--are you talking about using theoretical z/b values? Why not compute actual selection differentials and use these?

DR. TOUCHBERRY: Well, I suppose you could.

DR. HARVEY: Even for the incomplete records.

DR. TOUCHBERRY: What I was talking about was of all of the daughters dropped, how many completed records, and I don't see that we actually know how much selection was practiced.

DR. HARVEY: Well, do you expect that there is very much that they know about the ability of these heifers before they calve anyway?

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DR. TOUCHBERRY: No, no, I'm not speaking of culling before calving.

DR. HARVEY: So for a proportion of those that calve--

DR. TOUCHBERRY: If we could divide those not completing records into two parts, in one group would be those where the man had nothing to do with the heifer leaving the herd. I think that the size of this is in a sense a measure of whether this bull is carrying undesirable genes that cause animals to leave the herd; in the second group would be those that the dairyman knew something about, and says that he did cull this animal on the basis of production; this indicates that the bull has had some daughters that were very low producers.

If we assume that the natural losses vary little from bull to bull, then the fraction of daughters born that failed to complete a record is a rough measure of culling practiced, and the larger the fraction the more the index should be regressed toward the mean. In cases where a bull has a sizeable fraction of daughters culled after 1 or 2 months of lactation the resulting index should certainly be regressed whether or not the records are extended and included in the index.

DR. FREEMAN: Well, on the other hand, a lot of this is largely automatic. It is largely automatic in the sense that the bulls whose daughters aren't producing as well go out faster, and the bull also has a lower estimated breeding value.

DR. TOUCHBERRY: Yes, but not quite as low as it should be.

DR. HARVEY: Not if the breeder is pretty shrewd and knows how to cull.

DR. FREEMAN: Well, that is what I am saying. The culling makes it automatic.

DR. HARVEY: No, the ones that he has left that we measure are good cows. The ones that he has gotten rid of, that we don't have any records on, are no good.

DR. FREEMAN: Only provided that he got rid of them before they calved.

DR. HARVEY: Well, how about those that milked only one or two months?

DR. BENSON: What about culling before the first test?

DR. FREEMAN: Oh, yes, if you don't use those, I agree; I agree.

DR. HARVEY: But that is a pretty good measure.

DR. FREEMAN: But I think that they should be used, though.

DR. TOUCHBERRY: I think that they should be used, but it is just a matter of how they should be used.

THE CHAIRMAN: Dr. Touchberry, I realize that you weren't talking about this particular line, but I wonder if you or anyone else would comment on this: we all agree that not enough sires are being sampled; is the fact that we have the two million cows enrolled in recordkeeping in any way a serious limiting factor, at the present time, to genetic progress, through sire evaluation programs?

DR. TOUCHBERRY: I don't think that the two million cows limits progress, I think that it is the use of the older proven bulls, relative to the use of the younger bulls, that is the limiting factor. Many dairymen try to avoid using young bulls.

DR. VAN VLECK: I don't think it is either, on the population as a whole. But for the non-Holstein breeders, I think it probably is. There we are talking about a much smaller population.

DR. MEADOWS: Well, if we use the term "operation," operationally it is a hindrance.

DR. VAN VLECK: Right.

DR. MEADOWS: Because the simple reason is that if we had complete control of the population, we have plenty, but when we have to deal with many herds, we find some that will cooperate and some that won't operationally. So, I would say that we could sample many more bulls if we had many more herds on test, and I am not worried as much about how much of the cow population is used as how many people we operate with.

DR. HENDERSON: How long does it take us to get a Guernsey sire sampled?

DR. MEADOWS: Well, why don't we say Holstein? We have problems here.

DR. CARTER: We have Holsteins that take well over a year before they are adequately sampled.

MR. RUMLER: I think that this is something that the whole group has to take into consideration, as well as the AI people, that once you

start taking the economic incentive away from the breeders, you may not have as many cows to test as you have now under standard DHIA. You are constantly operating on the assumption that your testing programs are going to increase--and I hope that they do. But I think that without an economic incentive in standard DHIA, many breeders will be just as well off in the Owner-Sampler program. I think this is a factor that we have to keep in mind, and it comes back in effect, to what you said a minute ago.

DR. MEADOWS: I think this is an area where I will be in disagreement with the Breed Associations, in that they tend to look at the testing program as a matter of sire sampling. I would say that this represents, in rough figures, one tenth of the herds in Michigan on test. The economics comes from the management aspect and not the sire sampling.

MR. RUMLER: Well, I agree with that, but what I am saying is that you can get the management records from Owner-Sampler just as well as you can from a standard DHIA.

DR. MEADOWS: You won't like for me to say this, but I can get the breeding information from Owner-Sampler about as well, too. If I could just get the sire and dam identified. But I believe on this basis they would just as soon stay on standard DHIA.

MR. RUMLER: Well, this may well be, but I think that these factors must come into consideration so far as our research is concerned, with the approach that we recommend to be taken, because if the direction that we are going to set here, in the course of this group of people which are the genetic leaders of the industry, it is a course that undoubtedly will be followed. If it is all along one particular line, then this has to be the sure line to guarantee us that we are going to have to have enough economic incentives throughout the industry to accomplish in the light of the basic data that we use that we don't want to eliminate that particular factor in our consideration; because if we do it may be the most significant thing, more significant than other factors that we are considering now.

DR. MEADOWS: Well, I am quite sure that the biggest drawback to Owner-Sampler records from a breed improvement or change in the population standpoint is the failure to identify parents. For this reason, I made a little speech at your meeting that they ought to all be recorded. And I would say that we lose more information from failure to identify the dam or sire, either one, even in our DHIA program. So the real drawback would be the identification of the parents, rather than the number of cows on test. If they were all registered, we would have plenty of cows on test for our purposes.

DR. LEGATES: What percentage of our DHIA cows on test identified by either the sire or dam?

DR. MCDANIEL: I am sorry to admit that I don't know. We have a file there with about three million records without sires. Roughly, between sixty and seventy percent of the records reported to us have sire identification.

DR. TOUCHBERRY: There are probably enough on test where the sire is not identified to carry out a sire testing program.

DR. CARTER: About fifty percent of DHIA cows in New York are registered and, of course, have parent identification. If we don't have dam and sire, we call them grade. And then, unfortunately, among our grades, we have a little less than half of the sires identified.

DR. TOUCHBERRY: We need more cows on test, but we definitely need more complete pedigree information on those that are tested.

DR. MCGILLIARD: And this is the other place where counting the proportion that drops out before test is a serious problem, because identification is not continuous from birth.

DR. TOUCHBERRY: Right.

DR. MEADOWS: Just get them all recorded, and we will be under way.

MR. RUMLER: We have got to get a return from testing.

MCGILLIARD: This identification is a particular problem when we try to maintain identification from birth until sometime later. In Michigan, we have a system where calves are supposed to be identified at birth, even the grades, and they carry a control number through until their freshening. Well, they get one control number when they are born, and perhaps then the tester forgets about this and gives them a different one when they freshen, and then they are two different animals!

DR. FREEMAN: Or else they are eartagged or something, and the tag is just simply lost when they are a calf.

DEVELOPMENTS IN PHYSIOLOGICAL GENETICS

R. D. Plowman[a]

In recent years, genetic variation has been discovered in several proteins and review articles are available describing these polymorphisms (1,35,39). Some of the more important genetically controlled polymorphisms in cattle are blood groups (25,26,41), serum transferrins or β-globulins (7), hemoglobins (40), β-lactoglobulins (3), α_{s1}-casein (43), and β-casein (2). There is evidence to indicate that genetically controlled variation also exists in the milk protein α-lactalbumin, k-casein, γ-casein (2,42,13), and the serum proteins slow a_2 globulin (8,20), haptoglobulin (27), thread protein (4), post-albumin (20), acid phosphatase (20), and alkaline phosphatase (14). For most of this later group, however, the findings are preliminary and further work is needed to confirm the hypothesis of genetic control.

Blood Group Factors

Blood groups in cattle have been studied for almost 20 years. As a result much is know about the genetics of blood antigens. Eleven different linkage groups have been discovered. Although the mode of inheritance is simple, the genetics of blood groups in cattle is extremely complex because of the tremendous amount of variability found.

Blood Group Factors (45)

A System

A_1, A_2
D
H
Z'

B System

B, B_2
G
I, I_2
K
O_1, O_2, O_3, O_x
P
Q
T, T_2
Y_1, Y_2
A'
B'
D'
E', E'_2, E'_3
F'
G'
I'
J'
K'
O'
Y'

C System

C_1, C_2
E
R
W
X_1, X
L

F System

F_1, F_2
V_1, V_2

J System

J
O_c

L System

L

M System

M_1, M_2

N System

N

S System

S (H')*
U_1 (H')*
U_2
H'

Z System

Z, Z_2

R' System

R'
S'

* The H' is listed in parentheses to indicate that in cattle blood there is almost invariably an H' reaction along with either S or U_1. This does not necessarily hold true if cattle blood typing reagents are used on blood from other species.

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Several workers have attempted to study possible relationships between blood group genes and economically important traits. They are reported here by blood group systems.

A-System. Tolle (44) reported that cows with A_1 produced significantly more milk, but milk with a lower percent fat than cows lacking A_1. In 1963 (45) he again indicated a significant association between A_1 and superior milk yield.

B-System. Because of the many multiple alleles in this system, it is the most important locus for most cellular antigen studies including parentage verification. To date, more association studies have been tried with this system than with any other. Four different investigators have found an association between BO_1Y_2D' and superior fat test. Andresen et al. (10) found a statistically superior 0.07% increase in fat test for animals having this blood group. Rendel (37) indicated a superiority of 0.16% for animals with the same genotype. Neimann-Sorensen and Robertson (34) and Conneally and Stone (18) found significant increases in cows of 0.064% and 0.33% respectively as compared to other cows lacking this allele.

Two investigations, Andresen et al.(10) and Neimann-Sorensen and Robertson (34) found that the allele GD' was associated with high fat percent. These same two reports revealed that $O_1T_1E'_3K_1$ is associated with low fat test.

Hogreve (23) suggested that the B-system factor E_2^1 is linked with inferior lifetime performance.

Nair (33) reported a significant association between $BGIO_1T_2A'_1$ and low fat test in a group of Ohio herds.

Rendel (37) indicated that cows which were heterozygous at the B locus had a significantly higher fat test than cows which were homozygous at this system.

Tolle (44) reported that the B locus factors Y_2 and I^1 are associated with superior milk yield; that factor B is linked with inferior milk yield, and that the factor Y_2 is also connected with low fat percent--all of these associations being statistically significant. In 1963 Tolle (45) again reported the Y_2 factor and superior milk yield association to be significant.

J-System. The only reports in this system, Rendel (37,38) indicated that animals with cellular J produced milk with a higher fat percent than those animals with no J.

L-System. Rendel (37) reported that the L gene had a strong depressing effect on the fat percent of milk.

M-System. In this system there is excellent agreement among research workers of the association found. Mitscherlich et al. (31), Tolle (44,45) and Hogreve (23) working independently, all reported a highly significant association between the factor M and inferior milk production. Rendel (37) found that cows with M produce milk with a higher fat percent than cows lacking M.

S-System. Tolle (44,45) reported a significant association between the V_2 allele and inferior milk yield. Hogreve (23) indicated that this same allele and inferior lifetime performance are associated.

Z-System. A highly significant association between the Z factor and a depressing effect on milk yield was reported by Tolle (44). Conneally (18) found that cows heterozygous for Z gave more milk than homozygotes.

Serum beta-globulins (Transferrins)

Serum transferrins have been shown to be controlled by four autosomal alleles without dominance. They have been designated Tf^A, Tf^D1, Tf^D2, Tf^E. In recent years the phenotypes of this system have been studied to determine associations with economic traits.

In 1959, Ashton (6) reported a discrepancy in the expected numbers of offspring of various transferrin types from reciprocal matings involving Tf^A and Tf^D alleles. There were significantly more calves with types like their dams than those with types different from their dams.

In a later study of possible relationships between transferrin type and fertility in Australian cattle, Ashton (7) failed to confirm his original findings. He found, however, that conception rates were significantly higher in matings between homozygotes than in matings involving heterozygotes. The same results were found with English cattle (35). On the other hand, workers in Czechoslovakia (30), Denmark (16), Ohio (36), Sweden (21), and Wisconsin (19), have failed to find any significant relationship between transferrin types and fertility. Hickman and Dunn (22) studied nonreturn data on bulls used in artificial insemination in New York. Their data failed to confirm Ashton's findings of

highest reproductive performance in matings between homozygotes. However, their data do support the general hypothesis of a relationship between transferrin types and fertility, since some bulls with different Tf genotypes had significantly different nonreturn rates and there were indications that unlike mates were at a reproductive advantage. In their most recent paper on this subject, Ashton and Fallon (9) again report that conception rates are highest among homozygotes, especially those homozygous for the same gene.

Ashton (5) has also studied relationships between transferrin types and milk production. He studied 130 bulls used in artificial insemination in Great Britain and classified them according to their transferrin genotype. He found significant differences between groups of bulls of three transferrin types in the average production of their daughters as measured by the contemporary comparison method. The average contemporary comparison values were: Tf^A/Tf^A(A/A bulls, + 12.2 ± 6.9 gal, Tf^A/Tf^D(A/D) bulls, + 26.8 ± 5.4 gal, and Tf^D/Tf^D(D/D) bulls, + 38.2 ± 5.5 gal. Ashton also studied fat tests of 144 individual cows that were transferrin typed. There were no striking differences but there was a tendency toward higher fat tests in cows having the Tf^E allele. Ashton estimated that the transferrin locus accounted for 16% or more of the genetic variation in milk production. Robertson (39), however, points out that this value is too high and that 4% is a more realistic estimate.

At Wisconsin, Datta and Stone (19) failed to find a significant relationship between transferrin type and production in 215 Holstein-Friesian cows. Brummerstedt-Hansen et al. (16) stated that their studies of Danish cattle also failed to indicate a relationship. At Ohio, Rausch et al. (36) reported that cows not having the Tf^E allele gave more milk than cows with the other allele.

The most recent study was reported by Young and Hunter (47). They expressed first lactation milk and fat yields of 214 Holstein cows as deviations from herdmates. Intra-sire regressions of deviation milk and fat yield on number of transferrin D alleles were -309 and -9.1 kg. respectively. Gross means for the 39AA, 99AD and 76DD cows involved were +465, +331 and +172 kg. for deviation milk and +17.5, +12.9 and +11.5 kg. for deviation fat respectively. This study indicates a strong association between the transferrin alleles and production.

Hemoglobin

Hemoglobin variants are controlled by two alleles without dominance designated HbA and HbB. Hemoglobin B has been found only in certain kinds of cattle. These are Algerian and certain French breeds, Jerseys, Guernseys, Brown Swiss, South Devons, and Nigerian and East African zebu cattle (11, 16, 24, 28, 29, 40). The A type was also found in each of these kinds of cattle. In other breeds, such as the Holstein-Friesian, Ayrshire, Angus, Hereford, Shorthorn, and Icelandic cattle, only the A type has been found (11,15,40). Bangham and Blumberg, from their studies on African cattle, believe that there may be some association between Hemoglobin B and resistance to trypanosomiasis (11). Additional information is needed to provide a thorough understanding of the hemoglobin polymorphism and its maintenance in cattle.

β-Lactoglobulins

β-lactoglobulin has now been reported to be controlled by four autosomal alleles without dominance. They have been designated Lg^A, Lg^B, Lg^C, and Lg^D. The A and B genes are the most prevalent with the other two alleles being quite rare.

Aschaffenburg and Drewry (3) measured the amounts of β-lactoglobulin and casein produced by 24 cows of various β-lactoglobulin types. They found that among cows producing about the same amount of casein those of β-lactoglobulin type A/A produced about twice as much of the whey protein as B/B cows. Hererozygotes appeared to be intermediate. Moustgaard et al. (32) reported significant differences between cows of the different β-lactoglobulin types in casein content and β-lactoglobulin content of their milk. There was no difference in total protein content, however. Their data indicated, in agreement with Aschaffenburg and Drewry, that A/A cows produced more β-lactoglobulin than B/B cows and that A/B cows were intermediate.

Observations at Beltsville (42) indicated no difference in total protein yield of milk from A/A, A/B, or B/B cows. Thatcher (42) studied the relationship between predicted breeding value of AI proven bulls with 50 or more daughters and β-lactoglobulin type. Forty-seven bulls were available with known types. Daughters of A, AB, and B bulls produced on the average +500, +244, and +22 pounds of milk as compared to herdmates.

Other Milk Proteins

Association studies have not been made on other milk protein variants. Their genetic control, however, has been determined and is as follows:

Protein	Locus Symbol	Genes (Variants)
α-Lactalbumin	La	La^A, La^B
α_{s1}-Casein	α_{s1}-Cn	α_{s1}-Cn^A, α_{s1}-Cn^B, α_{s1}-Cn^C, α_{s1}-Cn^D
β-Casein	β-Cn	β-Cn^{A1}, β-Cn^{A2}, β-Cn^{A3}, β-Cn^B, β-Cn^C
k-Casein	k-Cn	k-Cn^A, k-Cn^B

Summary

It has been said by many workers that blood grouping has only a very limited value in predicting the breeding value of an animal as compared to the information obtainable by more conventional methods. Their reasons for this are that these characters are controlled by the genes of a large number of loci. Consequently, each gene can have only a rather small influence. Further, these characters are greatly influenced by the environment, so that the variation due to genetic factors is only a part of the total phenotypic variance. If this is true strong relations between blood groups and characters of economic importance can hardly be expected.

Many of the mentioned loci are independent of each other, suggesting that they are located on different chromosomes. As a result of this, these loci can serve as tools for the elucidation of the inheritance of characters, which are controlled by loci on the same chromosomes. It is possible that the blood group genes can be used as markers of genes controlling characters, which are not easily detectable or are detectable only in adult animals. In this case the blood groups will be of value for the cattle breeder as an aid in selection.

The milk protein polymorphisms and blood serum transferrins are relatively new and further work is needed to determine their usefulness in determining genetic value of animals. To the opinion of various scientists, neutral genes do not exist and the existence of these polymorphic systems does raise the question as to what mechanism is causing and maintaining the existing genetic diversity.

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CONTEMPORARY COMPARISONS

J. E. Legates [a]

I appreciate the chance to be here and participate in the discussions. We will try to talk around or about the subject of contemporary comparisons and perhaps the questions will become more direct after we get into the question session.

I haven't taken the complete title that was assigned, and I suppose that the first thing that I say is, "What is true?" We are always saying "true breeding value", and I always ask, "Do you have a false breeding value?"

I think that the first thing we need to define is what we mean by "contemporary" and I am drawing this in contrast to the term "herdmate", as we commonly use it. By contemporary we mean those animals that are born, essentially, at the same time and also freshened during a specified period. When we speak of herdmates the only restriction is that the animals freshen during a specific period of time in a given herd, but they may belong to different generations or periods of time.

So we will omit one word and just call it "contemporary" versus "herdmate". Now "contemporary" is, of course, conventionally followed with the terms of "first lactation contemporaries" although I think if we had sufficient second lactation animals and others, the contemporary concept could be extended to them.

There is a bit of a dilemma, if you consider our operational programs. It seems that those who are using herdmate comparisons are not quite satisfied with that, and those who are using the contemporary comparison are a bit uneasy about this procedure.

To start with, certainly I will say that the question is not clear cut. There will have to be some judgements made. All of the information we need isn't available yet. We have not really been working directly in this area at North Carolina, and so I am going to have to cite some work that Dr. Hickman and his group, and Dr. Allaire and Dr. Gaunt have pursued along with some general information that has accrued as we have observed this point over the years.

Now, the countries of Great Britain, and of course, Canada and Israel, are probably the major ones that are using what we would call a "contemporary comparison". In Canada, age adjustment to the breed class average is used, but in Britain and Israel the actual records are used. These countries follow a little different procedure, but in general, they are comparable to the traditional British scheme. Both in Britain and Israel the entire span of a year is included, rather than breaking it up into segments or parts of a year.

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Of course, in the United States age correction is much more readily accepted, and so we have moved into using all records, even from the very beginning, when we started with the daughter-dam comparison back in the thirties.

As I said, all of the advantages do not clearly lie with one or other system. I think it is important to emphasize the points that are advantageous and disadvantageous to the herdmate proposition, which we are using now, versus the potential alternative of the contemporary comparison.

Well, the first point is quite simple. Is there a difference between the mean of the contemporaries versus the herdmates? The problem might be stated in terms of how the method is implemented in the sire evaluation program that is conventionally used, and as Dr. Henderson has developed.

We come to the adjusted daughter record, based on the 305 day-2X-M.E. production record of the daughter, adjusted for the herdmates. The regression coefficient we use for our adjusted herdmates ($\overline{H}$) minus the rolling breed average ($\overline{RB}$) is .9. If we look at it from the point of view of contemporaries vs. herdmates, this adjustment (the .9) might be different. Assuming it is the same, we would be using then the contemporary herdmate average minus the mean, so the real difference that is involved is the regression times whatever difference there would be, between all of the herdmates and the contemporary herdmates. Is there any difference between these?

We say that our age factors are based on gross comparisons and, of course, they include an effect of selection, that is, the average effect of selection at the time of the data collected for the compilation of those age factors. If this has been changing, say, in five years, then these would not even adequately represent the average effect. When many herds are included, we expect these average effects of selection to be balanced out, or to approach the mean. If sub-groups or regions of the population are involved, there would be the possibility of a discrepancy that wouldn't be taken care of by this trend.

Now, first, on the second page of the handout material, I point out some of the information that raised the point in our minds as to whether or not some additional study was needed. This came from a comparison of AI and natural service progeny when Lee Tucker was with us. In the middle of page 2, and this was a comparison within herd, the standard contemporary proposition where each herd comparison was weighted according to the conventional British and Canadian procedure, the inverse of the variance of the particular comparisons. These comparisons are based on first lactation daughters that were availavle, natural versus AI. Then in the second line we use "herdmates", considering all individuals that were freshened.

The numbers are small, but the difference is 90 pounds of milk and 2.4 pounds of fat depending on whether we are using the contemporaries or herdmates on the same AI daughters, you see. These are identical AI daughters. This created a little interest to see what there might be in other situations.

Later we had another sizeable group of data -- these were HIR data. They were largely herds that had been using their own sires, the same group of data that Dr. Barr was talking about earlier, and they are not really comparable to the data from which our AI proofs are obtained. But they were available and we were interested in looking at the difference between first lactations and all lactations. These values do not take into account our regression to the breed average. This is just the difference -- not weighted -- of first lactations, and then comparing all lactations in the same season and pooling these on a contemporary basis with a weighting factor $n_1n_2/(n_1+n_2)$ for the individual herd-seasons that are involved.

Now these were looked at, as you can see, in four different regions of the country. In the North Atlantic region, with a sizeable number of records, there was a difference between the first lactations and all lactations of about 400 pounds. Moving on to the Midwest, you see just the reverse was true. The plus 53 means that the first lactations are superior to the average of all animals in the herd. Then, moving out to the Far West, for which the number of records is less, but still sizeable in terms of the standard error of the difference, there was a deviation of plus 222 pounds. Again, you see that the first lactation animals were exceeding all animals in this particular area. In the South there was a small number of records, but reflecting the same trend as in the Northeast in which the first lactation animals were below all animals.

Pooling these for the entire country, it was rather surprising that this difference was again about nine pounds of milk. The thing, however, that doesn't add much comfort is that we do have a real suggestion of regional differences. Why they are there, we don't know, but this is just the evidence. They appear to be of such a magnitude that you can't just dismiss them.

Now the range among herds is also rather wide, as we might expect, and these herds had a minimum of twenty records. There were a few of these herds, I believe, that were not on test for the full period from '53 to '59, but I believe all of them had at least four years. Our extreme values probably would be associated with the smaller herds, and the ones that were not on test for the entire period covered by the total data.

But these relationships do vary considerably from herd to herd. We have not investigated this further because this information really came out ancillary to another study. At this point we do not know why we have these regional and herd differences in the relationship of first lactations to all lactations.

This is something that we want to throw out as a problem which needs further clarification, especially in data that are used in our sire proving scheme. There may be others, but I should point out that Dr. Allaire and Dr. Gaunt looked at this in New England. They found a difference of about 250 pounds after it was regressed by about eight-tenths. Apparently there was about a 300-pound difference between first and all lactations in the New England area. That was for a period roughly comparable to the time of the HIR data -- 1956 to 1959, I believe. So their difference there would be minus 300, as compared to the minus 400 we have here.

Now, why does this come about?

We have already talked about age correction factors, and this is the first thing that I suppose one would suspect. It is difficult to tie down just how much is due to that, but I think that we need to recognize that we are making a comparison of first versus all; you have about three-quarters of the lactations that are by cows with second, third, and later lactations. So making a comparison of first versus first, the contemporary basis does minimize the impact of discrepancies in age factors on this difference that we get between the individuals that we are comparing and the contemporary average, as compared to herdmates. I don't think we need to dwell more on that other than to recognize it.

Another point is whether or not the selection in these various herds is of a differential nature. This would be a function of their culling practices, as well as herd expansion. Some herds are decreasing in size, but most of them are expanding.

We also have variation in the emphasis in different herds on different traits. Some are culling on production, and others apparently just bringing in replacements. To my knowledge no one has studied how these selection differentials vary from herd to herd, and what things are responsible for the variation. But it appears, at least, in what we have been able to look at, that they are variable from herd to herd.

There are essentially three things that could contribute to this difference, plus or minus. The third one is what we want to measure, the genetic merit of the sires of the two groups of cows being compared. We wouldn't want to tamper with that, but we would like to rule out as far as possible the effect of age factors, and also the undue influence of any selection bias, if this is a factor.

These are the key points that I want to present as possible factors to consider in revising our operational approach to the sire evaluation system.

Now we have followed the problem a bit further. Some of you may know that we work with a somewhat specialized group of herds in our North Carolina Institutional Program. Since 1949, we have had a small pilot breeding program going with those herds, in which there are now about 700 milking cows.

At the time we were looking at Lee Tucker's contemporary comparisons for the AI versus natural service study in North Carolina, this 90 pound difference came up, and we became interested in seeing what was happening in our herds. At that time we did take a look at the comparison of first versus all lactations. And, in our group of herds, we had a difference of minus 352 pounds of milk and minus 8.4 pounds of fat. Any three of these points previously mentioned might be involved in varying degrees. Three or four years ago, we compiled the summaries on the first twenty-three

young bulls that had been in the sampling program, and these were compiled on the basis of comparing their first lactations to all individuals, and then a contemporary comparison. Twenty-two out of the twenty-three were lower in their first lactation comparison when we used all herdmates as versus using contemporaries.

When we went through the standard procedure that is used in DHIA, our difference for these sires in their overall proof was minus 379 lbs. milk and a minus 7.4 lbs. fat. In other words the proof on first lactations would be this much higher, as compared to using the same first lactation records, but comparing them with all herdmates.

Just recently, looking at those cows that had at least one record and which were still in the herds, there was a superiority based on first lactation deviation of about 450 pounds of milk.

This is a sizeable amount if we are comparing a young bull to an older bull. Now the thing that is quite difficult to assess is what amount of this potential bias is really involved on the average. The maximum you get is when you are comparing a bull that has only first lactation daughters to a bull that has daughters with several lactations, and we don't have that in all cases. If we had bulls that had only first lactations, the full impact of it would be expressed if we used all lactations of herdmates. At the present time we would say that the strictly contemporary comparison should be a better estimate, not taking into consideration the precision of the herdmate average.

Let D be the discrepancy and N be the average number of records per daughter. If N were one the full impact would be felt. But as we increase the average numbers of records per daughter this would be reduced, assuming that we do not have a bias when we compare these later records.

As we move onto more records, the impact of any selection or age conversion errors would diminish. If we are comparing bulls that have only one lactation versus those that have an average of two, you see, we would have approximately half of the discrepancy, contributing to the comparisons between them. In some cases older bulls' daughters may have an average of three or more lactations, but not many would have more than that. Probably the upper limit would be D vs. D/3.

It seems to me that those are the factors that will be responsible for any systematic difference between comtemporaries and herdmates. These are age conversion factors, differential culling of older cows, the residual of what culling has taken place, and then the merit of the sires.

We do not want to tamper with the merit of the sires, since this is the thing that we would like to examine. So we would like to use a procedure that would, in a practical way, minimize our age factor discrepancies, and take care of this differential culling.

The bias is not quite a constant for any region, nor is it constant for any particular herd, which makes the question more difficult to resolve.

Culling bias has been considered in another manner, just considering the number of records. The central question is what is the tangible difference between the first lactation cows and those cows that are a residual of the culling. In the western states the older animals were poorer cows, so there was a net negative selection differential. There was no positive relationship between the number of additional lactations and the selection differential.

We need to utilize procedures that would take care of these effects, but in so far as possible leave our sire effects undisturbed.

There probably are other ways, but the most direct possibility, it seems to me, is to make use of our contemporary comparison. This should minimize these effects considerably. We would be comparing first lactations of all animals and this is probably as unselected a group of animals that do have records available. So this is one of the reasons why one might lean in favor of the contemporary comparison.

There are some things that probably cause us to hesitate to accept this procedure. One of the first things is a reduction in the number of contemporaries. We have a possibility of a loss of information if certain of the daughters do not have contemporaries when we restrict ourselves to first lactation individuals.

Here again I am just going to draw on some information that Dr. Hickman and Dr. Gravir have published.

As I said, the Canadian group is one of the groups that is investigating whether they ought to shift to the herdmate comparison. They have made a study to see how many contemporaries are available under their scheme. This study included data for a two-year period, and their herd size at that time was about twenty lactations -- distributed reasonably uniformly between the two seasons which they use.

A key point, it seemed to me, was that of the total first lactation animals in the Canadian data, about 7.9 percent had no contemporaries. This would be a little higher percentage, possibly 10%, if you took out paternal half sibs from the contemporaries. Now their herd size is considerably smaller than we have in the United States. As Dr. Hickman mentioned, it is smaller than theirs is now, although Canadian herd size has not increased as rapidly as ours in the United States.

The other information on this point comes from Dr. Allaire and Dr. Gaunt. They studied this in New England and looked at two intervals: one was a seven-month period, and in the second they included eleven months. When they worked with the eleven-month period, there were just over five contemporaries for first lactations. For the seven-month interval, there were four-plus contemporary first lactation animals available. Increasing the interval from seven to eleven months only picked up one other individual. When all herdmates were used the number was about 13, on the seven-month basis.

Now there are other things that I should bring out, and this I may need correction on:

It appeared from their data that about two percent of the animals had no paternally unrelated herdmates. On the seven-month basis there were about 6.6 percent with no contemporaries. With the eleven-month interval, there were 4.6 percent with no contemporaries.

This is the only evidence on this point I know of -- maybe there are others -- where we have some picture as to the number of individuals that would lack either contemporaries or herdmates.

An additional point is that for a given herd size there will be fewer complete lactations reported than the number of cows, generally. You can get more records including incompletes than the average number of cows.

The herd size, when the New England data were collected, was 40.1, as contrasted to the Canadian situation which was 20, and as of the last DHIA report, the herd size in these three States has increased to 50.2. We have ten more cows per herd now than when these data were obtained. In the United States as a whole, we were at 39.9 at the time that their data were collected, and at the present time it is 52.9, with a wide range, of course, because of Florida, and particularly, California. I think that we are still very close to fifty plus, even in our concentrated dairy areas.

Now in addition to this complete lack of contemporaries, as I said before, we also have a difference in the number of contemporaries. So we have the matter of precision in estimating the contemporary average, and then, carried further, the sampling variance of our difference. There are expressions which give us the theoretical expectation of this variance. But there are a lot of insidious relationships between herdmates and between non-related individuals, so that I feel that these theoretical expressions would need to be paralleled with an empirical study to assess the number of contemporaries or herdmates that are needed. Is four adequate? Five? Ten? Or do we need thirteen?

Well, again Dr. Allaire and Dr. Gaunt should be up here since I am dwelling on their work. They computed the variance of contemporary averages for three cases, and also the variance where you would pool the records, as we conventionally do. Say the cows had two or three records, and you get an average for contemporaries, based on all of the herd-seasons that were included.

The thing that is surprising is that the estimate of the variance of the contemporary average had pretty well diminished down to the magnitude of the herd component by the time they had four or five contemporaries. It appears on this sort of superficial look at it, at least, that going for a tremendous number of herdmates or contemporaries is not so important.

Presumably, after we have four or five contemporaries we have got most of what is there to reduce -- this is just the variance of the contemporaries or herdmates. We might suspect this, if we look at our weights; as one n_2 take on values of 1, 2, 3, 4, and so forth, the weight

$$\frac{n_1 n_2}{n_1+n_2}$$

becomes one-half, two-thirds, three-fourths and four-fifths, and then five-sixths. These would be the w_i

$$\frac{n_1 n_2}{n_1+n_2}$$

In the simple daughter-contemporary comparison, the weight approaches one very rapidly, so that when we get up here to nineteen contemporaries or herdmates, the weight is .95. Looking at it in this way indicates that after we had four, five, or six, that we perhaps had done most of what could be done.

While we are going to have fewer contemporaries than we are herdmates, I would say that we need not worry about getting an unduly large number, in terms of contemporaries and herdmates. It is the number of daughters that are available that is the most important.

DR. HENDERSON: A figure that I have here on herdmate comparisons verifies this even more so. The variance is in the range of 1.6 for one herdmate, to a limit of 1.2.

DR LEGATES: In the other?

DR. HENDERSON: A very large number of herdmates.

DR. LEGATES: Right. At least, the point, I think, is clear that there is no necessity in our comparison to have an unduly large number. We have been printing this listing, and, I suppose, have been looking at twenty and thirty herdmates as adding a lot more reliability than it actually does. And my feeling is that if we have four, five, or six, or certainly up to eight or nine, there isn't much need of worrying about this point. This, I believe supports the feasibility of the contemporary comparison in contrast to herdmates.

Now, what are we going to do about it? Or what should we do about it?

Well, for one possibility, I have separated off first lactations and later. Now you can break them down; some would prefer first, second, and you can go on down. The reason that I have done this -- and we can argue about this operationally -- is that the first proof is our most important proof, and the first proof is almost exclusively on the basis of first lactations. You may have a few scattered daughters that might have a second and third. Later on you might have enough individuals to try a second lactation contemporary comparison.

In our North Carolina institutional herds, where herd size is large, since about 1960, we have followed a scheme that has not been worked up too rigorously, in which we start with first versus first, and then second and later lactations versus the second and later. Rather than deciding on what particular weight is to be given to these two potential proofs that you have on a bull, we have merely pooled them.

Apart from the fact that first lactations are the immediate basis for our judgement on a bull, and that a bigger share of our judgements must be made on them, we are beginning to observe some of the peculiarities of first lactations. This raises the question of what kind of goal we ought to set in our breeding program, and what this true breeding value is that we are seeking.

Do these first lactations have sufficient uniqueness that we might want to get a proof on first lactations? And then we could combine the second and later, and then, by employing a selection index procedure we could put these two measures together.

Barker and Robertson have suggested this possibility: Roughly, about a quarter of our lactations are first lactations, and three-quarters are by later lactation animals. One might say, of course, our milk production in actual pounds is more by later lactation animals, so our rule of thumb might be that the weight for the first lactation proof might be one, and three for the others. This does not consider the economics of producing herd replacements.

Now quite a number of the heritability estimates published are beginning to show a difference between first and later lactations. The British and also the Europeans on the Continent have published several reports. There has not been so clear a suggestion of this in the U.S. data, as we have had from some of the overseas reports.

I noticed in the material that Dr. Freemen presented yesterday, that there was a difference between the heritability for first and later lactations for milk, in which it dropped considerably from about three-tenths to about two-tenths, from firsts to seconds. And I don't know why that happens exactly.

DR. FREEMAN: Well, there are not as many numbers in those later lactations. We also did this on a lot of ABS data from the West Coast, and actually, there were very small differences, with the second lactation heritability being the highest.

DR. LEGATES: The seconds were the highest? Well, as I say, this is something for which we do not have the full answer. It varies back and forth. But there are enough reports showing differences that we begin to have suspicions.

Now the other point is that the genetic correlations between first lactation, and second, and third, are high, but not unity.

Dr. Freeman seems to have the lowest values that I have run across in relating first and later lactation in the Iowa Institution herds. But in the estimates that Van Vleck and Barker and Robertson have obtained more recently, there seems to be a genetic correlation of about .95 between firsts and seconds. The correlation between first and thirds drops down to maybe eight-tenths, and seemingly, the estimates of the correlation between the two's, three's, and four's, where they are available, seem to cluster and be more unique.

We need to look at this more. But there seems to be some reason for us to consider a first lactation proof on the genetic basis of the question. Now we could build into this, of course, the number of daughters and so forth, in regressing the proofs according to their reliability.

These are the major ideas that I would put out. I think that the question in our total population centers on the availability of contemporaries. On the evidence we now have it looks as though we wouldn't lose a great deal, because we are already losing two percent of our daughters as it is. This would tend to decrease, because our herd size is increasing. We don't need a tremendously large number of herdmates, although this needs re-verification. We also are making our major judgements on the basis of first lactation records.

I believe that we come closer to eliminating the problems of selection and age factor discrepancies if we use some function of first lactations or use contemporaries rather than all herdmates in our comparison procedure.

There is one other possibility that maybe I will just throw out:

For those of you who are associated with bull studs, it seems to me that we might consider a proof on a first lactation basis over a short period of time. In our institutional stud, we are able to take about a two-year period, animals freshening during a two-year period, and encompass the bulls that we are interested in looking at for nomination for entry into full service. Taking that two-year period of first lactations, we then pick up a new crop of the established bulls. And generally your established bulls have considerably more daughters, even in return usage, than the bulls that you are making your first judgements on. So the accuracy of your judgement, in ranking these bulls, using just first lactation information, is not greatly affected by the reduced number of daughters of your older bulls.

The point that one would need to consider carefully is whether this second sample of the daughters coming in from these older bulls that have previously been proved are as representative of these bulls as their first daughters were. The effect of genetic trends would be minimized also.

This is all I have to say. I will just leave it up to you for discussion. I have talked around the problem and now I will let you ask the questions and see if we can get some answers.

DR. FREEMAN: We have done a good bit more work on this, and it is not in print yet, and so maybe I should mention it. Also, I think there is

an abstract at about '59 or '60, based on the Institutional herds, although they were very small numbers, particularly for second and third lactations.

DR. LEGATES: You are referring now to the --

DR. FREEMAN: Heritabilities of first, second, and third.

DR. LEGATES: And genetic correlations?

DR. FREEMAN: And genetic correlations. Well, we recently took another look at this -- I forget exactly, but it was somewhere in the neighborhood of 100,000 lactations from the West Coast, and another two or three hundred thousand from the Midwest.

And to make a long story short, when you pooled the results over the whole thing, if you assumed that the values that we got were the true parameters, for firsts, seconds, and thirds, and comparing this against using an average of all records, the gain would be in the neighborhood of two percent for first, second, and third lactations, if you weighted them individually versus using an average. So there was not a whole lot here in our data.

DR. HENDERSON: Well, I think that this is the same result that Andy Lee found.

DR. FREEMAN: The only place that I think would even conceivably warrant doing it, if you were sure of the parameters, would be in making selections of individual cows for special matings. There could be a little bit of gain here. But even so, the statement that I made was assuming that those parameters that we estimated were the true values.

MR. RUMLER: Dr. Legates, how would you rank the values of the two methods in, say, a single herd proof, where you may have a large number of daughters of a single bull and, say, perhaps a limited number of daughters of other bulls, freshening at the same time?

DR. LEGATES: Of course, we would like to have these contemporaries or herdmates representing a random sample or a representative sample of all bulls in which we are interested. And in the single herd proofs, this presents a problem.

MR. RUMLER: So you couldn't compare them?

DR. LEGATES: I suppose that there would be a bit more justification for including more individuals in single herds. You would be pooling the proof over seasons, but you probably wouldn't have more than a couple of seasons for your first proof on a bull.

MR. RUMLER: Well, do you think it would probably be less valuable than a herdmate comparison?

DR. LEGATES: Well, I am still not overly concerned with getting a large number of contemporaries and throwing in a lot of correlations among your contemporaries that you don't know about. You might have such a

[illegible] 500-mm TOA, based on [illegible] small models, particularly [illegible]

[illegible] reforesting [illegible]

[illegible] first, second, [illegible]

DR. LEGATES: [illegible]

DR. FRENKIEL: Anticyclonic corrections. Well, [illegible] look at this. -- I know exactly [illegible] 100,000 lapsed [illegible] the [illegible] used for the Midwest?

And to make [illegible] when you predict the [illegible] ship, if you [illegible] the [illegible] tors, for [illegible] and [illegible] radiosonding this against [illegible] age [illegible] all records, this again [illegible] the neighborhood of two pressure [illegible] to arrive, to weight [illegible] us using an average. So there was [illegible] whole lot [illegible]

DR. [illegible] Well, I [illegible] that this is the [illegible]

DR. FRENKIEL: [illegible] only place that I think [illegible] conceivably [illegible] use of the parameters would be in moving [illegible] for spectral analysis. There [illegible] be a little [illegible] even so, the [illegible] that I made [illegible] that [illegible] were the [illegible]

MR. BUNDGAARD: [illegible] you [illegible] the values [illegible] say, a single hard [illegible] large [illegible] a single hard, say [illegible] frequency [illegible] the same [illegible]

DR. LEGATES: [illegible] sources, we would like to have [illegible] contemporaries [illegible] sources are random [illegible] preprocessing [illegible] which would [illegible] in the [illegible] [illegible]

[illegible] So you [illegible]

[illegible] I suppose that there would [illegible] but [illegible] transition [illegible] would be positive [illegible] you probably [illegible] more than a sample [illegible] first [illegible] a bulk [illegible]

[illegible] Well, do you think it would possibly be [illegible] valuable [illegible]

[illegible] I am [illegible] lot [illegible] don't know [illegible] might [illegible]

diversity of culling practices that the difference which I have suggested between first and all lactations might be quite variable.

In your situation you have only one herd. With AI we have a chance to reduce this down to about 100 lbs. This is the difference between first and all lactations.

MR. RUMLER: But I am thinking only of these two-year old records.

DR. LEGATES: I still am more in favor of going to the "true contemporaries", even though it needs to be checked further. But I lean that way.

MR. RUMLER: Yes, but are you speaking now of single herds?

DR. LEGATES: Yes.

MR. RUMLER: Even though they may have, for example, ten daughters of one bull and there may only be five daughters of other bulls?

DR. LEGATES: Yes, we talk about these, but I think that George pointed out that in general the number of sires used is rather large. You have a number of herds that are jointly using AI and their own bulls. More and more, the situation is going to become less acute, rather than stay even as bad as it is now, in terms of the number or sires represented among the herdmates.

And now, granted, it is not going to be ideal. It is not strictly ideal in our AI situation. It approaches this. This is just an opinion that I have and it needs to be checked, certainly. But I still lean even in single herd situations in so far as numbers will permit, to using the true contemporary approach.

DR. FREEMAN: What was the rank order of bulls evaluated in the two ways?

DR. LEGATES: I don't have enough information to even give a picture on that. Do you have one?

DR. McDANIEL: Dr. Fairchild has worked on this problem.

DR. FAIRCHILD: I have a study that was carried out about three years ago. I have a few figures that more or less substantiate some things given already. I know that Dr. Allaire and Dr. Gaunt found what they call a selection bias of about 258 pounds. And my results agree with your figures, where we had four regions of the country. In the Midwest it looks the other way around. I have ten pounds -- plus ten pounds, or something like that. I don't know whether it is age correction, or a matter of the young sires looking so much better.

DR. LEGATES: You do confirm the regional differences, then.

DR. FAIRCHILD: On the six-month season basis, I had 4.4 percent that did not have contemporaries.

[illegible] I suspose that the difference which I have suggested

[illegible] have only one head. With AI we have a chance to reduce this down [illegible] 100 lbs. This is the difference between fires and all incendiaries.

MR. [illegible] I am thinking only of these [illegible] old records.

DR. [illegible] are in favor of going to the "zero and zero varies", even [illegible] pushed further. But I feel that [illegible]

DR. [illegible] are speaking now of single heads?

DR. [illegible]

DR. [illegible] they have [illegible] example, ten daughters one bull and [illegible] five daughters or other [illegible]

DR. LEGATES: Yes, we talk about these, but I think that George pointed out that in [illegible] number of sires used is rather large. You have a number of herds [illegible] jointly using AI and their own bull. More and more, the situation is [illegible] less acute, rather than stay [illegible] as it is now, in [illegible] number of sires represented among the [illegible]

[illegible] now, however, it is not going to be ideal. [illegible] is not strictly [illegible] in use AI [illegible] It approaches fidelity. This [illegible] opinion [illegible] I have and [illegible] certainly. [illegible] I still lean [illegible] single have attractivity [illegible] as numbers will permit. In using the [illegible] contemporary [illegible]

DR. FREEMAN: What was the rank order of bulls evaluated in the two [illegible]

DR. LEGATES: I don't have [illegible] give a picture on that. Do you [illegible]

DR. [illegible] AI [illegible]

ROOM: [illegible] a study [illegible] carried out [illegible] three years [illegible] Alliance [illegible] Canne Fondo [illegible] pounds. [illegible] by results agree with [illegible] places of the [illegible] In the Midwest [illegible]

DR. LEGATES: This was on a six months basis, yes.

DR. FAIRCHILD: Oh, and another thing that I found was when I used what you call the true contemporary comparisons, there was a disturbing sire-by-herd interaction.

DR. LEGATES: Yes, I didn't mention this -- have you an explanation of that? The point that he is mentioning here is that the sire by herd interaction component, where you use contempories, is magnified about two-fold, I believe, over what it is ordinarily. It is still disturbingly large, even using our herdmate comparison. It increases, as contrasted to unadjusted records. Have you looked into this at all, Dr. Van Vleck?

DR. VAN VLECK: I think that the results that we have got were stratified by year, so it reduces that.

DR. BURNSIDE: Claire Rennie and a student did a study on these two procedures. They looked at quite a number of sires, I guess, in the neighborhood of sixty to a hundred, and the rankings were very similar. The correlations were .8 to .9, with those numbers.

DR. LEGATES: So that the impact, as I want to say, is variable. If you have got a lot of herds, it is going to average out to pretty much the same. If you have a subset of the data, for example, regions, this is another proposition that needs consideration.

DR. BARR: Just in the way of description of these Holstein data that I described yesterday, I calculated the same kind of correlation among adjusted herdmate averages as I did among the dams, and the estimate that I got was .75. Just among the herdmates -- not really among the herdmate averages.

DR. FREEMAN: Part of that is because the same cows are teamed in adjacent herds.

DR. BARR: Right.

DR. LEGATES: Or adjacent seasons.

DR. FREEMAN: Yes.

DR. LEGATES: New records, but the same cows.

DR. McGILLIARD: If you are going to use the contemporary comparison, what is the argument against taking the next step and comparing the bulls only where we have daughters in the same herds that are contemporaries?

DR. LEGATES: I would have no argument with making the comparison. I am all for, as you say, designing it to begin with to do the kind of thing we desire, if we can do it reliably enough. Of course, Dr. Harvey and Dr. Henderson can perhaps give us the maximum likelihood scheme for the most efficient way of using all the records, rather than throwing any away.

[illegible] This was on a small number [illegible]

[illegible] Oh [illegible] something that I found [illegible] what you call [illegible] the contemporary comparisons, there [illegible] disturbing [illegible] average 100.

DR. EGATES: Yes, I didn't mention that -- have you [illegible] of that? The [illegible] that he is went [illegible] that [illegible] where you use contemporary, is something above [illegible] what it is ordinarily. It is [illegible] using [illegible] herdmate comparisons. It increases, in contrast [illegible] records. Have you looked [illegible] this at all, Dr. Van Vleck?

DR. VAN VLECK: I think that the [illegible] that we have [illegible] by [illegible] it reduces that.

DR. BURNSIDE: Claire Kennedy and a student did a study on these [illegible] looked at quite a number of [illegible] I guess [illegible] herdmates [illegible] to a hundred, and the rankings were very [illegible] .8 to .9, with those numbers.

DR. LEGATES: So that the impact, as I want to say, [illegible] If you have got a lot of herds, it is going to average out [illegible] pretty much the [illegible] If you have a [illegible] of [illegible] this [illegible] proposition that needs consideration.

DR. HAHN: Just in the way of description of these Holstein data [illegible] I described yesterday, I calculated [illegible] correlation among adjusted herdmate averages as I did among [illegible] estimate that I [illegible] Just among the herdmates -- not really among the herdmate averages.

[illegible]: Part of that is because [illegible] same cows are [illegible] adjacent herds.

[illegible]

"[illegible] records, [illegible] the same cows.

[illegible] are going [illegible] comparison [illegible] with the [illegible] in the same herds that [illegible] test"

[illegible] with making the comparison. I am [illegible] you [illegible] to begin [illegible] to do the kind of thing [illegible] Of course, Dr. Harvey and [illegible] likelihood [illegible] the [illegible]

As I understand it, Norway essentially does this. They breed a lot of daughters of a bull and then they only use those that match their proposition and try to do it with a minimum amount of age and season correction.

THE CHAIRMAN: On a contemporary comparison scheme, Dr. Legates would you advise the use of age conversion factors?

DR. LEGATES: Well, yes. I should have mentioned this. I think we definitely need some age factors. I would go along, if we could get it sold, and so as someone said yesterday, to adjust to, say, thirty months or twenty-seven months. This would further reduce these age discrepancies and probably cut down our interaction term, too.

DR. McDANIEL: I will just make one point, and that is that these regional differences that he showed here, the difference between first lactations and all lactations, is in the exact direction that we would expect based on the regional differences in age correction factors that we have found. And actually, your data, although HIR, are to some extent an independent set of data from what we used. But again the regional trend is identical.

DR. LEGATES: Yes, the West Coast would be more independent because California hasn't been reporting to DHIA.

DR. McDANIEL: Am I correct in thinking that the rank order of bulls and the repeatability of the evaluation would be key criteria in comparing the usefulness of the two methods?

DR. LEGATES: I would think it would be, yes. This rank order, what we would be looking at within a particular area, would it be different, if you were going to compare bulls across regions and so forth?

DR. FREEMAN: Well, I have got to be convinced of this, and I will tell you why:

We had this ABS data made in the San Joaquin Valley. They obtained initial progeny tests in a number of herds. I think that they had about seventy herds, all told. And at the time that these bulls were used out there, the data from California were not reported to USDA, and we correlated our estimates of the breeding value in the California herds with the USDA proofs, which were from data all over the country, but did not include the California records, and the product moment correlation between the two proofs was over nine-tenths.

DR. LEGATES: Well, of course, you expect this. You see, you have just two regions.

DR. FREEMAN: No, we have California versus the rest of the United States.

DR. LEGATES: Well, yes, but what I am saying is that this would still minimize the difference because the California bias would come out of its

mean, and the other includes a large area and obscures specific effects.

DR. FREEMAN: Yes, but the point is that the rank order correlations would have been higher than this, so I don't think these rank orders would show greatly differences.

DR. LEGATES: Well, I wanted to say that the differences could be magnified.

DR. FREEMAN: Well, that might be. But I have got to be convinced that they would be greatly different.

DR. LEGATES: With two particular areas, you can certainly minimize this interaction.

DR. FREEMAN: No, that is not a good general statement. It depends on what two areas you are talking about, if you are referring to an interaction.

THE CHAIRMAN: I am sure that there are probably other questions, but maybe we can pick them up a little later in the morning or this afternoon.

ESTIMATION OF BREEDING VALUES WITH LEAST-SQUARES AND MAXIMUM LIKELIHOOD TECHNIQUES

Walter R. Harvey [a]

Most of the theory and techniques to be discussed in this presentation have been published by Dr. C. R. Henderson and his co-workers. A list of the pertinent literature is given at the end of this paper. The primary purpose of this paper is to discuss briefly some of the basic problems involved in computing maximum likelihood estimates of breeding values and producing abilities when adjustment must be made for fixed environmental effects.

ONE-WAY CLASSIFICATION

When no adjustments are required for fixed environmental effects or if adjustment factors are used which are assumed to be perfectly accurate, the model reduces to the one-way classification model as follows:

$$y_{ij} = \mu + a_i + e_{ij}$$

$$i = 1,2,\ldots,p$$

$$j = 1,2,\ldots,n_i$$

Now if the intra-class correlation

$$r = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

or the ratio σ_e^2 / σ_a^2 and μ are known, the maximum likelihood (ML) estimates for the breeding values or producing abilities are

$$\mu + \hat{a}_i = \mu + \frac{n_i r}{1 + (n_i - 1)r}(\bar{y}_i - \mu)$$

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[a] Ohio State University.

where $\bar{y}_i$ is the simple average of all records for the ith animal. The ML estimates are unbiased in this case regardless of how the a_i are selected provided the records for each individual, whether they be different measurements of the same trait or measurements of the same trait on equally related family members, are randomly obtained.

If μ is unknown and must be estimated from the data two alternative procedures for estimating μ are available provided the a_i in the data were randomly drawn. The procedure to use depends on how the records on each animal are obtained. If the records on each animal or breeding group are randomly drawn but the number of records is correlated with breeding values or producing abilities one should use the least-squares estimate of μ, i.e.,

$$\hat{\mu} = \frac{\sum_i \bar{y}_i}{p} .$$

When the a_i are randomly drawn and the number of records is uncorrelated with the a_i one should probably use the maximum likelihood estimate of μ, which is the mean of the estimated breeding values or producing abilities rather than the mean of the simple class averages. However, the ML estimate of μ seems to be less reliably estimated than the LS estimate and also the LS estimate is an unbiased estimate of μ, in this case. Hence, there is some question as to whether one obtains the "best" estimates of the breeding values or producing abilities when μ and the breeding values are obtained simultaneously when r is known and the records and the a_i are drawn at random.

Fortunately, the rank correlation between estimated breeding values or producing abilities is high even though the two estimates of μ used differ considerably. Hence, in practice I would generally recommend the use of the simple average of all records or the LS estimate of μ when μ must be estimated from the data.

When the a_i and records are drawn at random one may obtain an unbiased estimate of r from the data in the usual manner. However, if the data are not numerous r will be inaccurately estimated and it will often be preferable to use an estimate of r from outside the data.

In order for the reader to follow the computational procedures more easily when adjustment must be made within the data for fixed environmental effects, let us consider for the one-way classification the following set of data:

Animal	Record No.	y_{ij}
1	1	11
	2	15
2	1	10
	2	6
	3	8

Now if

$$\mu = \frac{1}{2}\left[\frac{11 + 15}{2} + \frac{10 + 6 + 8}{3}\right] = 10.5$$

and r = .4, then

$$\mu + \hat{\hat{a}}_1 = 10.5 + \frac{(2)(.4)}{1 + (1)(.4)}(13 - 10.5)$$

$$= 10.5 + 1.43$$

$$= 11.93$$

$$\mu + \hat{\hat{a}}_2 = 10.5 + \frac{(3)(.4)}{1 + (2)(.4)}(8 - 10.5)$$

$$= 10.5 - 1.67$$

$$= 8.83$$

These estimated breeding values or producing abilities may also be obtained by setting up the usual LS equations, imposing the restriction that $\sum_i \hat{a}_i = 0$, solving the remaining equations and then regressing the LS constant

estimates for the a_i as follows:

<u>LS Equations</u>

$$\begin{pmatrix} 5 & 2 & 3 \\ 2 & 2 & 0 \\ 3 & 0 & 3 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{a}_1 \\ \hat{a}_2 \end{pmatrix} = \begin{pmatrix} 50 \\ 26 \\ 24 \end{pmatrix}$$

<u>Reduced LS Equations</u>

$$\begin{pmatrix} 5 & -1 \\ -1 & 5 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{a}_1 \end{pmatrix} = \begin{pmatrix} 50 \\ 2 \end{pmatrix}$$

$$\hat{\mu} = \frac{250 + 2}{24} = 10.5$$

$$\hat{a}_1 = \frac{10 + 50}{24} = 2.5$$

and,

$$\hat{a}_2 = -\hat{a}_1 = -2.5$$

Now,

$$\hat{\hat{a}}_1 = \frac{n_1 r}{1 + (n_1 - 1)r}(\hat{a}_1)$$

$$= 1.43$$

$$\hat{\hat{a}}_2 = -1.67$$

as obtained above.

when $\mu = 10.5$ and $r = .4$ the ML equations for the a_i are as follows:

$$\begin{pmatrix} 3.5 & 0 \\ 0 & 4.5 \end{pmatrix} \begin{pmatrix} \hat{\hat{a}}_1 \\ \hat{\hat{a}}_2 \end{pmatrix} = \begin{pmatrix} 5 \\ -7.5 \end{pmatrix}$$

where: $3.5 = n_1 + \frac{1-r}{r} = 2 + 1.5$

$4.5 = n_2 + \frac{1-r}{r} = 3 + 1.5$

$5 = 26 - (2)(10.5)$

$-7.5 = 24 - (3)(10.5)$

The solution of these two equations, of course, yields the same ML estimates of the a_i as obtained above. It is obvious that the right hand members of these equations would be different and hence the ML estimates would differ if a value for μ other than 10.5 were used. The value of μ which forces the $\hat{\hat{a}}_i$ to sum to zero is the ML estimate of μ and is obtained by solving the following three equations:

$$\begin{pmatrix} 5 & 2 & 3 \\ 2 & 3.5 & 0 \\ 3 & 0 & 4.5 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{\hat{a}}_1 \\ \hat{\hat{a}}_2 \end{pmatrix} = \begin{pmatrix} 50 \\ 26 \\ 24 \end{pmatrix}$$

The solution is

$\hat{\mu} = 10.31$

$\hat{\hat{a}}_1 = 1.54$

$\hat{\hat{a}}_2 = -1.54$

The estimated breeding values or producing abilities are 11.85 and 8.77 compared with 11.93 and 8.83 when the LS estimate of μ is used.

TWO-WAY CLASSIFICATION WITH NO INTERACTION

The model in this case is the same as for the incomplete block design with one replicate as follows:

$$y_{ijk} = \mu + a_i + b_j + e_{ijk}$$

$$i = 1,2,\ldots,p$$

$$j = 1,2,\ldots,q$$

$$k = 1,2,\ldots,n_{ij}$$

The computational procedure to follow in order to obtain the "best" estimates of the breeding values or producing abilities (the $\mu + a_i$) depends on the a priori information available and the characteristics of the data available. It will be assumed that the b_j are fixed environmental effects and that they must be estimated from the available data in all cases. In order for these estimates to be unbiased the records available on each animal (a_i class) must be distributed at random with respect to the different b_j classes.

When μ is Unknown and r is Known

When this condition exists one must then decide whether it is valid to assume that (i) the a_i are chosen at random from some population of a_i and that (ii) the numbers for the different a_i are distributed at random with respect to the b_j. If the first assumption is invalid no unbiased estimate of μ exists from the data. However, it is possible to obtain an unbiased estimate of μ and the b_j even though the second assumption is not true. A satisfactory estimation procedure to follow when μ is unknown, r is known, assumption (i) is true and assumption (ii) is false is as follows:

1) Set up the LS equations in the usual manner for the $\mu + a_i$ and the b_j. If the number of a_i is large the equations for the b_j may be set up on an intra-A-class basis, i.e., the equations for the $\mu + a_i$ are absorbed by LS. In this case, the estimate of μ may be obtained from the mean of the

$\hat{\mu} + \hat{a}_i$, which are computed with a back solution procedure, viz,

$$\hat{\mu} + \hat{a}_i = \frac{1}{n_{i.}} (Y_{i.} - \sum_j n_{.j} \hat{b}_j)$$

or an unbiased and often satisfactory estimate of μ may be computed more easily as

$$\tilde{\mu} = \frac{1}{n_{..}} (Y_{..} - \sum_j n_{.j} \hat{b}_j).$$

2) Compute the ML estimates of the animal breeding values or producing abilities as follows:

$$\hat{\mu} + \hat{\hat{a}}_i = \hat{\mu} + \frac{(1/C^{ii}_{\mu A})r}{1 + [(1/C^{ii}_{\mu A}) - 1]r} (\hat{a}_i)$$

where $C^{ii}_{\mu A}$ is the inverse diagonal element for the $\hat{\mu} + \hat{a}_i$.

If $\tilde{\mu}$ is used instead of $\hat{\mu}$, $\tilde{a}_i = \hat{\mu} + \hat{a}_i - \tilde{\mu}$. The regression coefficient in the ML formula may be written in terms of the variance components as

$$\frac{\sigma^2_a}{\sigma^2_a + C^{ii}_{\mu A} \sigma^2_e} .$$

Now if μ is unknown, r is known and assumptions (i) and (ii) are both true one can estimate the b_j more accurately by making use of the differences among the a_i which are confounded with the b_j as well as the differences among the b_j within the a_i classes. In addition, the ML estimate of μ may be obtained from the data. The estimation procedure is as follows:

1) Set up the ML equations.

	$\hat{\hat{\mu}}$	$\hat{\hat{a}}_i$	$\hat{\hat{b}}_j$	Y
μ:	$n_{..}$	$n_{i.}$	$n_{.j}$	$Y_{..}$
a_i:	$n_{i.}$	$n_{i.} + \frac{1-r}{r}$ (0 on diagonal, 0 off diagonal)	n_{ij}	$Y_{i.}$
b_j:	$n_{.j}$	n_{ij}	$n_{.j}$ (0 on diagonal, 0 off diagonal)	$Y_{.j}$

To solve these equations only one restriction or constraint is required.

A convenient restriction is that $\sum_j \hat{\hat{b}}_j = 0$.

It should be noted that one may absorb the equations for the $\hat{\hat{a}}_i$ into the remaining equations without absorbing μ with the usual absorption procedure. In fact, this is the procedure one would usually follow if the number of animals is large.

In this case the $\sum_i \hat{\hat{a}}_i$ will equal zero since these are now measured as a deviation from the ML estimate of the mean, $\hat{\hat{\mu}}$. The estimates of the breeding values or producing abilities are the $\hat{\hat{\mu}} + \hat{\hat{a}}_i$.

When μ and r are Unknown

When the variance components are to be estimated from the data it is necessary that the a_i be randomly drawn. However, it is possible to obtain unbiased estimates of the variance components by using Method 3 of Henderson even though the a_i are not distributed at random with respect to the b_j. In this case, the procedure to follow would be as follows:

1) Complete a method 3 analysis to estimate r. In the process of doing this one can, with little additional work, obtain the $\hat{a}_i$, $\hat{\mu}$ and the inverse diagonal elements $C^{ii}_{\mu A}$.

2) Regress the least-squares constant estimates to obtain the ML estimates of breeding values or producing abilities.

If one has considerable data and it seems valid to assume that the a_i are not only drawn at random but that they are distributed at random with respect to the b_j, one can complete an iterative ML analysis to simultaneously estimate the variance components and the fixed effects. The procedure is as follows:

1) Complete a method 3 analysis to estimate r_1.

2) Modify the LS equations for the a_i with $\frac{1-r_1}{r_1}$ and re-estimate the variance components from the ML sum of squares for A and its expectation.

3) Continue until the estimate of r and the fixed effects remain constant.

4) The ML estimates of μ and the a_i will be obtained directly from the last iteration.

Computational Example

Suppose the data given previously were also classified into B classes to yield the following LS equations:

$$\begin{pmatrix} 5 & 2 & 3 & 4 & 1 \\ 2 & 2 & 0 & 1 & 1 \\ 3 & 0 & 3 & 3 & 0 \\ 4 & 1 & 3 & 4 & 0 \\ 1 & 1 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{a}_1 \\ \hat{a}_2 \\ \hat{b}_1 \\ \hat{b}_2 \end{pmatrix} = \begin{pmatrix} 50 \\ 26 \\ 24 \\ 36 \\ 14 \end{pmatrix}$$

[illegible] analysis to continue [illegible]. In the process of additional work, obtain the [illegible] involve different elements [illegible].

Increase [illegible] iteration estimates of prevailing values or random [illegible] multiples.

One has considerable data and it seems valid to assume that the [illegible] drawn at random but that they are distributed [illegible] random [illegible]

[illegible] to the [illegible] one [illegible] complete an iterative ML analysis to [illegible] estimate the variance components and the fixed effects. The procedure is as follows:

1) Complete a method 3 analysis to estimate σ_μ^2.

2) [illegible] the ML equations for the [illegible] with $\frac{1-r_i}{r_i}$ and [illegible] estimate the variance components from the ML sum of squares for A and [illegible] expectation.

3) Continue until [illegible] estimate of [illegible] and the fixed effects remain constant.

4) The ML estimate of [illegible] the [illegible] be obtained directly from the last iteration.

In data given previously were also classified into 8 equations:

Imposing the restrictions $\sum_i \hat{a}_i = \sum_j \hat{b}_j = 0$ results in the following set of reduced equations:

$$\begin{pmatrix} 5 & -1 & 3 \\ -1 & 5 & -3 \\ 3 & -3 & 5 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{a}_1 \\ \hat{b}_1 \end{pmatrix} = \begin{pmatrix} 50 \\ 2 \\ 22 \end{pmatrix}$$

The solution to these equations is

$$\hat{\mu} = 11$$

$$\hat{a}_1 = 2$$

$$\hat{b}_1 = -1$$

with $\hat{a}_2 = -2$ and $\hat{b}_2 = 1$. Also

$$\begin{pmatrix} 5 & -1 & 3 \\ -1 & 5 & -3 \\ 3 & -3 & 5 \end{pmatrix}^{-1} = \frac{1}{12} \begin{pmatrix} 4 & -1 & -3 \\ -1 & 4 & 3 \\ -3 & 3 & 6 \end{pmatrix}$$

and $C_{\mu A}^{11} = \frac{4}{12} + \frac{4}{12} - (2)(-\frac{1}{12}) = \frac{1}{2}$

$$C_{\mu A}^{22} = \frac{8}{12} + \frac{2}{12} = \frac{5}{6}$$

Hence, when $r = .4$

$$\hat{\hat{a}}_1 = \frac{(2)(.4)}{1 + (2-1)(.4)} (2) = .571 (2) = 1.143$$

$$\hat{\hat{a}}_2 = \frac{6/5(.4)}{1 + (6/5-1)(.4)} (-2)$$

$$= .444 (-2)$$

$$= -.889$$

and the estimated breeding values or producing abilities are

$$\hat{\mu} + \hat{\hat{a}}_1 = 11 + 1.143$$

$$= 12.143$$

$$\hat{\mu} + \hat{\hat{a}}_2 = 11 - .889$$

$$= 10.111$$

Now if the a_i were randomly chosen and these effects are distributed at random with respect to the b_j effects one could do the ML analysis directly as follows:

ML Equations when r = .4

$$\begin{pmatrix} 5 & 2 & 3 & 4 & 1 \\ 2 & 3.5 & 0 & 1 & 1 \\ 3 & 0 & 4.5 & 3 & 0 \\ 4 & 1 & 3 & 4 & 0 \\ 1 & 1 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} \hat{\hat{\mu}} \\ \hat{\hat{a}}_1 \\ \hat{\hat{a}}_2 \\ \hat{b}_1 \\ \hat{b}_2 \end{pmatrix} = \begin{pmatrix} 50 \\ 26 \\ 24 \\ 36 \\ 14 \end{pmatrix}$$

One restriction is necessary in order to obtain a unique solution. When the restriction is imposed that $\sum_j \hat{\hat{b}}_j = 0$ the equations are

$$\begin{pmatrix} 5 & 2 & 3 & 3 \\ 2 & 3.5 & 0 & 0 \\ 3 & 0 & 4.5 & 3 \\ 3 & 0 & 3 & 5 \end{pmatrix} \begin{pmatrix} \hat{\hat{\mu}} \\ \hat{\hat{a}}_1 \\ \hat{\hat{a}}_2 \\ \hat{b}_1 \end{pmatrix} = \begin{pmatrix} 50 \\ 26 \\ 24 \\ 22 \end{pmatrix}$$

The solution of these equations is as follows:

$$\hat{\hat{\mu}} = 11.25$$

$$\hat{\hat{a}}_1 = 1.00$$

$$\hat{\hat{a}}_2 == -1.00$$

$$\hat{\hat{b}}_1 = -1.75$$

Since $\hat{\hat{b}}_1 + \hat{\hat{b}}_2 = 0$, $\hat{\hat{b}}_2 = 1.75$. The estimated breeding values or producing abilities are now:

$$\hat{\hat{\mu}} + \hat{\hat{a}}_1 = 11.25 + 1.00$$

$$= 12.25$$

$$\hat{\hat{\mu}} + \hat{\hat{a}}_2 = 11.25 - 1.00$$

$$= 10.25$$

It should be noted that the ML estimates of the b_j effects differ considerably from the LS estimates. This is very likely to happen when there are many a_i classes if the a_i effects are not distributed at random with respect to the b_j, i.e., the a_i and the b_j effects are correlated due to the way the data are collected.

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SIRE EVALUATION METHOD WHICH ACCOUNTS FOR UNKNOWN GENETIC AND ENVIRONMENTAL TRENDS, HERD DIFFERENCES, SEASONS, AGE EFFECTS, AND DIFFERENTIAL CULLING

C. R. Henderson[a]

Any method of sire evaluation is at best a compromise. Ideally we should like to write a model which describes accurately the factors that determine the magnitude of a production record. This model would include a description of the distributional properties of the elements of the model. In addition, we would hope to know the parameters of these distributions. Given this information, we could then derive the best method for ranking A.I. sires or even for predicting how well each of them would do in a given environmental situation. The facts are, of course, that we do not know the model and consequently can only state that if the model is as we describe it, the best prediction method can be found. Thus, the first compromise has to do with our statement of the model rather than the actual model. The second compromise is one of practicality. The best method may be too expensive or too time consuming computationally. These costs must be balanced against what we can hope to gain over using simpler methods.

I propose to present here a tentative model which is, assuming that we know certain ratios of variances, the best sire evaluation method under these assumptions. The computational methods clearly are difficult, and they may not necessarily be put into routine use, but rather may serve as a guide to more efficient methods than are now available.

When you see what model is implicit in the present herd-mate method, I think you will agree that we may be rapidly approaching a time when changes in methods will be imperative.

Consider the model of A.I. and non-A.I. herd-mate records:

$$Y_{ij} = \mu + h_i + 1/2\, g_i + s_j + e_{ij}$$

$$X_{ik} = \mu + h_i + g_i + e_{ik} \quad ,$$

where Y_{ijk} is the record of one A.I. daughter of the jth sire in the ith herd-year-season (hereafter this will be called herd).

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X_{ik} is the record of the kth non-A.I. daughter in the ith herd.

h_i is a herd environmental effect

g_i is a herd genetic effect

e_{ij} , e_{ik} are random errors

h_i , g_i , e_{kj} are normally and independently distributed with means=0.

$\sigma_e^2 / \sigma_h^2 = 1.25$

$\sigma_e^2 / \sigma_g^2 = 5$

Now suppose that in the ith herd there is only one A.I. daughter and there are n non-A.I. cows (herd mates of the A.I. daughter).

When μ is known, the best estimate of s_i, assuming sires fixed, is the solution to the following equations: (See Henderson, Selection Index and Genetic Advance, NRC Publication, or Henderson, et al., Biometrics, 1959.)

$$\begin{bmatrix} 1 & .5 & 1 \\ .5 & n+5.25 & n+.5 \\ 1 & n+.5 & n+2.25 \end{bmatrix} \cdot \begin{bmatrix} \hat{s}_i \\ \hat{h}_j \\ \hat{g}_j \end{bmatrix} = \begin{bmatrix} y_{ij} - \mu \\ 1/2(y_{ij} - \mu) + (X_{i.} - \mu) \\ (Y_{ij} - \mu) + (X_{i.} - \mu) \end{bmatrix}$$

The solution to $\hat{s}_i$ is

$$(Y_{ij} - \mu) - .9 \frac{n}{n+1} (\overline{X}_{i.} - \mu)$$

Note that this quantity is exactly the herd-mate adjusted daughter record as used in the New York method for many years. The average of such adjusted records, regressed according to the number of progeny, was

the sire evaluation method used in practice. More recently we have modified the method to take into account the number of records on each daughter in such a way as to eliminate bias due to differential culling.

Relative to the results above let us state some of the assumptions implicit in this model.

1. All records are adjusted for age without bias.

2. There is only one A.I. daughter in each herd.

3. $\sigma_h^2 + \sigma_g^2 = \sigma_e^2$

4. $\sigma_g^2 / (\sigma_h^2 + \sigma_g^2) = .2$

5. All herds are a random sample from a single hypothetical population. This implies that there is no trend due either to environmental or genetic causes.

6. The herds are assigned at random to the A.I. sires subject to the restriction of one daughter per herd.

7. The A.I. sires used are a random sample from a single population. This implies no time trend of sire genetic values.

It is obvious that some or all of these assumptions are untenable in the present situation. At the time the herd-mate method was developed they were more reasonable assumptions. Further, the computing facility then available was an IBM 602A, thus simple models leading to simple techniques were mandatory. Now however, with rapid changes occurring in dairy and A.I. industries and with the availability of tremendously improved computing facilities, it is time to consider possible drastic changes in methods.

I should like therefore to propose a model that is more realistic and to describe a computational procedure that assumes this model.

Let us consider now some of the probable difficulties in our present methods. First, we are assuming in this procedure that we have a single population, within a breed, of sires eligible for use in A.I. and then

we take a random sample of sires from that population for actual use. If we are talking about a set of contemporary bulls, I think that it is quite all right. But if we are evaluating sires that have been put in service over a period of ten or fifteen years, and if we are making any progress at all, this is not a single homogeneous population.

We might have a situation such as Dr. Harvey was talking about, or maybe a combination of random sires about a fixed trend, or we have sire groups of some kind. One can define those groups any way one chooses in terms of when the bull came into service, the region in which he is used, etc. Any realistic method, under present conditions, must account for the fact that an obvious genetic trend is occurring. We must surely abandon the concept of a single population from which we have a random sample of sires, unless we are concerned only with contemporary sires. So I would like to change the model to the extent of having sire groups of some kind.

Now another assumption that could be questioned is that herd-year-seasons are a sample from a single population. Obviously there are positive correlations between herd-year-seasons all in the same seasons, between herd-year-seasons all in the same herd, etc. The present procedure assumes that these are uncorrelated variables. There have been reasons, partially computational and partially a question of trying to get smaller sampling variances, for making these assumptions in the past, however. I am not trying to excuse what we have been doing. I am just saying that there are reasons for what we have been doing. If herd-year-seasons are not, in fact, a random sample about some single mean, but instead we have a situation in which herds are actually random samples about a mean which has been changing, then this requires a different procedure and a different model. We now have a situation, of which most of you are aware, that daughters of sires recently entering A.I. service are being compared with herd-mates that are better than the herd-mates would have been had the sire entered service at some earlier period. Where sires stay in for a long time each new crop of daughters is being compared against a different set of herd-mates--better herd-mates than the ones with which previous sets of daughters were compared. This leads to the observation that sires which stay in service for some time appear to be decreasing in breeding value. I believe that any ideal sire evaluation procedure would yield a stable evaluation for a sire with many daughters. I think that we have given the dairyman the impression that when a bull has a large number of progeny we know his breeding value. However, in our reports we appear not to know what we are talking about--we appear to keep getting variations in estimated breeding value of the same bull. In terms of ranking bulls which are contemporaries, I do not think this is too much of a problem.

We also see the result which Dr. McDaniel mentioned, as created by season-age interactions. If a bull happens to get a large crop of daughters coming in during a bad season for the young animals, this makes him appear to take a sharp drop if he has had a previous crop in a better season. Then he will tend to go back up if the next set of daughters freshen in a good season.

So I think that the things that we really need to try to take into account in sire evaluation, would be, as a minimum, genetic trends and environmental trends. Both of these are unknown, but, undoubtedly, a combination of the two exists because record averages have been going up dramatically.

We know, very definitely, that we have herd differences, part of which are genetic and part of which are environmental. We know that the trend in individual herds is not the same as the overall trend. So we have year-by-herd interaction and year-by-season-by-herd interactions.

We also have the overall seasonal effects, and we have age effects, which are confounded with seasonal effects, and possibly to a lesser extent with the long-time trends. I believe that our data indicate that we don't have nearly as marked effects of age-by-year interaction as we have of age-by-season.

If we are going to use more than first records, we have the age effect problem, and we also have the problem of differential culling. So it seems that we should use a procedure which would take into account all of these effects simultaneously; genetic and environmental trends, culling, and age effects.

Now a little aside on age-effect estimation:

Dr. McDaniel pointed out the biases that are present in both the gross comparison method. John Beardsley, with my advice and help, attempted simultaneous estimation of genetic trend, environmental trend, and age effects, and came up with very sensible age effects, which I believe the Jersey Cattle Club is still using. But if you look at his detailed results, you find some very wild genetic trends; I forget whether they were dramatically upward or downward. The environmental plus the genetic trends was sensible, about equal to the actual trend in production as you might expect, and the age estimates appeared to be all right, although one does not really know. But the separation of the genetic trend from the environmental trend was obviously not accomplished.

One wonders what the reaction would have been had the age effects been very peculiar looking and the genetic and environmental trends had appeared sensible-say that two-thirds of the trend was environmental and one-third was genetic, which might have been quite palatable and acceptable. But if sensible environmental and genetic trends had been found, the age estimates would no doubt have been peculiar looking. Fortunately, Beardsley got "good" estimates of age effects, the main purpose of the study.

Now the basic problem, as I think some you know, is that if we had the situation of each cow calving on the same day each year; that is, if you had a twelve-month calving interval, and then if we classified ages according to years of age, and we classified genetic groups, as I suggested in an American Dairy Science Association meeting paper in 1949, according to date of birth of the cow you can see that, so far as any cow is concerned, if you know which age group, or which year of birth group she is in, and also know her age, you then know the year in which she made her record. Or taking any two of these, you automatically know the third variable.

Consequently, there is no way of getting a solution to age effects, environmental trends, and genetic trends, using repeated records on the same cows, if we have the simple situation of the one-year calving interval. Now we do not, in fact, have this. We get equations in which the confounding is not perfect and a solution could be obtained if we had a computer with unlimited word length, but the coefficient matrix will come close to singularity, and the solution is certain to be of very little value. This is a problem that deserves much attention in working with "messy" data and complicated models.

Most matrix inversion programs or programs do not check very well for singularity of the coefficient matrix, and because of rounding errors you can get "solutions" to equations that really have no solution. Thus we have the very unpleasant situation of not being able to estimate age factors, if we assume that both genetic and environmental trends are present.

I do have some confidence that we now may have discovered a method for estimating simultaneously age factors and genetic and environmental trends. The trick in this is to use sire groups and dam groups as the genetic groups, rather than individual cows, since there is less confounding of these with age and year of freshening than there is between a cow's own year of birth and for age and year of freshening.

Now I shall proceed to some details of the simultaneous estimation of many factors. This, obviously, will require excellent computing facilities, and that one not have to pay too much per hour for this during the developmental period. Availability and costs of computing facilities will certainly determine the feasibility of my suggestions. I think we could handle the problem in our situation at Cornell, with a 360 Model 40 having 128K memory and with off-hours time available for research.

If you have to rent the equipment it may not be feasible. Now I will have to admit again, as I was saying at the outset, that one sometimes bends the model, to some extent, to fit the computational facilities available.

I do not like a few assumptions in the model, but I think that if we do not use them the model is completely impossible from any practical computational standpoint. Well, the elements of the model then, which I have considered, are first of all, years. These would not necessarily be calendar years; they might well be "fiscal" years, depending upon when heavy freshening occurred--I would suppose, probably, a year beginning in July or August, so you wouldn't be splitting December from the January freshenings. And then, because we do have season-age interactions, I have suggested here that we have a classification of season-age groups.

Now I don't know how many seasons would be required. I think, from some of my own work, that probably two seasons in the New York data or the Northeastern data would probably be all right with a 7-5 split. When did the five month period begin, in August, Dr. Carter, do you remember?

DR. CARTER: September.

DR. HENDERSON: But this is quite arbitrary, and it would depend on how one thinks that it really should be set up. Of course, one would like to have as few groups as possible, from the standpoint of the number of equations involved, so one would, obviously, not have age groupings by one-month intervals when you get up to, say, cows at forty-eight months. It could be one-month intervals at the lower ages, and then a segment by two-month intervals, and then later on by six months, and then by years. So you try to reduce the number of groups to some manageable number, but it would still be, I suppose, in the order of a couple of hundred age factors that you would be estimating.

Then I have suggested dam groups, and it might be feasible or desirable to have two different kinds of dam groups: the natural service dams that were got, as Alan Robertson, would say, by natural service; and those who were by A.I. service. I chose to throw them all together, but one would not have to do so. You could define these dam groups in any way that you would want. You could have groups of A.I. dams born in a given year or who had their first daughter, or were themselves born in a given year; that is, some classification to take into account the possibility of trends in the genetic merit of the dams whose daughters make the records.

If you wanted to introduce regions, then you would obviously have in region one the dams born in a given period of time, in region two the dams born in that same period of time, and you would have the unfortunate situation of never having a direct comparison in the same herd between dam group of region one with a dam group in region two, and this would mean that the estimates of differences between regions would probably not be very good or possibly not estimable at all.

Also I have suggested that we have natural service sire groups, and also A.I. sire groups. I think that it is highly important to have these separated, because the evidence is that there is a fairly dramatic difference between the progeny of the two groups, and it seems to be getting wider, year by year. All of the evidence in the Northeast would indicate that this is what is happening, when we make comparisons between natural service daughters and A.I. daughters in the same herd. The comparison is biased somewhat in favor of the natural service group, in that if we do not know the sire, we say that the animal is non-A.I., so there are some A.I. sires in the so-called natural service group. Also, of course, there are many natural service sires who are the sons of A.I. sires, so there is some A.I. influence in them. The procedure I am presenting provides still another method of estimation of the differences between A.I. and non-A.I. and this new procedure would presumably do this with a little less confusion from age factors, differential culling, etc.

So we have the classification for A.I. sires, and that, of course, is one of the things that we are really after, to evaluate the A.I. sires. These would be random effects, but keep in mind that they would be random about their own group mean, so that A.I. sires would be a random set of sires with respect to the sub-population of which they are a part.

And then we have herd effects, and here are two things that I don't like about the model--I don't know whether to call herds fixed or random,

and also, it is distasteful to me to merely say that we have a herd effect and to neglect the possibility of herd-by-year and season interaction. I have done the latter for a very definite reason, purely computational. If we do not, we are in almost an impossible predicament, unless we want to use only first lactation records. I would like this in many respects, because life becomes far more simple since we then can use herd-year-seasons, regard them as fixed, and be in a very pleasant situation computationally. The only difficulty is the question as to whether we want to evaluate sires on the basis of first lactation daughters alone, and this is a question that has not really been settled.

Next, the model contains individual natural service sires. Data from natural service sires can be used to decrease the sampling variance of our estimators, and additionally can be used to estimate the breeding value of these sires themselves. As was mentioned yesterday, these estimates of breeding value are valid only if there is no differential treatment of some kind. But ignoring differential treatment, we get the best estimate of the breeding value of natural service sires by taking into account any comparison that we might have between them and a well-known A.I. sire that is tested in many herds. You then have a good measure of that natural service sire if the possibility of differential treatment can be ignored. The question of preferential treatment is always going to be the burden on the user himself, because this cannot be determined from the data.

DR. FREEMAN: May I ask a question here? Could you clarify the distinction between A.I. sires and A.I. sire groups? I take the A.I. sires to be those you are interested in estimating their breeding value?

DR. HENDERSON: These are all sires which have been used going back a certain period of time, however far back you want to go, and these are all A.I. sires that have produced daughters or have records in the herds that we are dealing with.

DR. FREEMAN: All right, now how about the A.I. sire groups?

DR. HENDERSON: I am not quite sure how these would be classified. It could be on the basis of when their first daughter freshened, or when the sire was born--I will leave it up to you as to how to group them, but some kind of a grouping which would take into account the time trend in the merit of the A.I. sire population.

DR. HICKMAN: The same sires, or the A.I. sire group?

DR. HENDERSON: We have nesting of a group of A.I. sires within each of these groups, and each of the sires within the group is regarded as a random individual from this sub-population. The sub-populations presumably are different.

DR. TOUCHBERRY: These are the A.I. sires then, those within the groups?

DR. HENDERSON: Yes.

DR. MOXLEY: You have got two classifications here--the A.I. sire groups and the A.I. sires, and I was just wondering whether the A.I. sires are, in fact, the sires that you divide into groups, to get your other classification?

DR. HENDERSON: Well, let us say that the A.I.G. that we are estimating is actually a mean, and we don't have all of the sires from that population. We have a sample from the population. I don't know how you would define this population exactly. This is the same problem that we have in any genetic analysis in that we have to conceive of some population from which we have a random sample.

DR. FREEMAN: But, in fact, the A.I. sires, when re-classified, do make up the A.I. sire groups?

DR. HENDERSON: Yes, they make up all of these, those which contribute anything to the sire group comparison.

DR. MEADOWS: So you are just estimating sires between the groups?

DR. HENDERSON: Right.

DR. HARVEY: But aren't you really saying that there is no basis for comparing sires from group to group?

DR. HENDERSON: No, we will be able to compare them from group to group, because we will have an estimate of the group mean. For example, to compare sire 5 in group 1 with sire 9 in group 2, we compare

$$\hat{AIG}_1 + \hat{s}_{15} \quad \text{with} \quad \hat{AIG}_2 + \hat{s}_{29} \quad .$$ I think that this is important. Otherwise, we are not making a fair comparison between a sire that came into service ten years ago, compared to a present one.

DR. HARVEY: Just look at the deviation within group then.

DR. HENDERSON: Yes.

DR. FREEMAN: But adding the group means with the group adjustment.

DR. HENDERSON: Yes.

DR. HARVEY: The group means were taken out?

DR. HENDERSON: No, the group means are taken into account, and are the estimates of sires within a group are relative to this group mean.

DR. HARVEY: They are regressed toward the group?

DR. HENDERSON: But then the group means are used in the comparison of sires that come from two different groups. Now I think that it is very important to regress toward group means rather than a general mean. Otherwise we are assuming that there has really been no trend.

DR. GAUNT: Essentially, this sire group could be a different year?

DR. HENDERSON: It could be. And also, if you wanted to bring in region, you could do that also.

DR. McGILLIARD: Aren't you likely to have a problem of confounding between groups of dams and groups of sires, though?

DR. HENDERSON: Yes, to some extent.

DR. McGILLIARD: Is this going to bother you?

DR. HENDERSON: No, but I will have to admit that my thinking is biased rather considerably by what we could do with our data from the Northeast, and how far you could extend it to a nationwide program, I am not really certain. I think that the confounding between sire groups and dam groups would be far from complete within our own situation, and we can get good estimates of both of them.

DR. McGILLIARD: Yes.

DR. HENDERSON: You will have somewhat of a cluster of numbers here on the diagonal, but not complete diagonality so you can get estimates of all of the sire groups. The thing that you have got to watch, if the data extend over a long time, is that you might get complete confounding.

DR. HARVEY: Well, you are saying that there is no time trend between the dam groups and the A.I. sire groups, or vice versa, which may not be true. In other words, you are making a very coarse grouping. To begin with, it was a grouping by time distribution or something of the A.I. sires, but are you saying that there is no trend within the group?

DR. HENDERSON: Oh, yes, within the group, right.

DR. HARVEY: And, therefore, this could be used to help estimate dam effects?

DR. HENDERSON: Yes.

DR. HARVEY: It could bias that, if there really was a trend present.

DR. HENDERSON: Yes. I am also saying as I have presented it here, that there is no interaction between sire groups and dam groups and, in fact, I have ignored a number of interactions, for better or for worse. The more I have worked with dairy records, the less I like to use very many interactions in the model. We almost always get a wild set of estimates, if we introduce many interactions.

DR. McGILLIARD: In actuality, with unequal numbers, is there any meaning to the definition of general effects and interactions?

DR. HENDERSON: Well, I don't want to get into this question because this gets back to discussions that I have had with some of Dr. Lush's students over a long period of time, and I don't think that we quite understand each other on this. You and I may, but I am not sure about it. There is some confusion between models and the pattern of sub-class numbers. Actually the <u>model</u> is independent of subclass numbers, but the <u>estimates</u> are not.

DR. HENDERSON: Is there anything else about the model that anybody would like to ask? It simply appears to be an operational model for our facilities, and it would take into account a lot of things which are not now taken into account.

MR. RUMLER: You said this would require 128 K storage capacity?

DR, HENDERSON: That is what we have, yes. I think we can do it with a computer of that size.

DR. FREEMAN: Does it bother you at all when you consider that you could call effects fixed or random, depending on how you handle it?

DR. HENDERSON: The only real question that I would have about fixed or random effects would be herds. Years, I certainly want to regard as fixed.

DR. FREEMAN: Well, this question would bother me a little. I don't want to belabor a point, but in terms of, say, sire groups with culling fixed, there is no logical reason for saying that those in years one and two constitute a group, why couldn't they constitute a group in two and three?

DR. HENDERSON: Oh, this is quite right.

DR. FREEMAN: This problem would bother me.

DR. HENDERSON: If you knew the real trend, what I would really prefer would be random effects about some known trend. In fact, if we don't know the trend, I just think that it is somewhat easier to divide it arbitrarily into groups.

DR. McGILLIARD: Am I correct that in using fixed and random you are going to specify the point around which these things vary?

DR. HENDERSON: Yes. Now, regarding whether herds ought to be fixed or random, the computational procedures are so similar that it doesn't make any difference. That is, the computational aspects of it do not enter in. It is a question of whether our estimates are going to be biased worse one way or the other. Now it is true that if we regard herds as random and if there is correlation between the genetic merit of the herd and the genetic merit of the sire used in that herd, biases will result as Dr. Harvey pointed out. So, from the standpoint of avoiding that bias, one had better regard herds as fixed. On the other hand if we do not have such correlations, we get larger sampling variance by regarding herds as fixed than by regarding them as random. I think that I would prefer to pay the penalty of a higher sampling variance to avoid bias.

Those of you who heard my paper at Michigan last year may realize that if herds really are random, and if a herd passing out of existence depends upon the production of that herd up to that point, then not regarding herds as random may bias some of the other fixed effects.

DR. HARVEY: Of course, there is another problem that comes in here If sires interact with herds, or sires interact with years, you are trying to predict something in the future for other years. And in other herds that are not yet in the data. Then you have to regard these effects as random, from that standpoint. Either that or forget about it.

DR. HENDERSON: Or assume that the interaction doesn't exist, yes. I think that, operationally, we proceed with, and if one had a computer with unlimited memory and speed, you could store this set of maximum likelihood equations in the memory of the machine as you read your data in, and then solve the resulting equations, and these equations would contain equations for years--say, ten years--season, age groups, perhaps two or three hundred, dam groups, numbering 10 to 20, natural service sire groups, the same number, A.I. sire groups, about that number. A.I. sires of the Holstein breed would number about what, Dr. Van Vleck?

DR. VAN VLECK: About 500, at least.

DR. HENDERSON: With one or more daughters?

DR. VAN VLECK: Oh, more than that.

DR. CARTER: For how long a period?

DR. HENDERSON: I don't know. That would make a difference, wouldn't it? Well, let us say 1,000 A.I. sires, just to indicate the magnitude of the problem here. How many herds have we had in DHIA in the Northeast in the past ten-year period?

DR. CARTER: We are talking DHIA now, and in samples, A.I.--

DR. HENDERSON: No, also natural service. It would be several thousand anyway.

DR. CARTER: We are processing 10,000 herds.

DR. HENDERSON: So I will say 15,000. Natural service sires, how many per herd did we say? Someone gave the number of natural service sires per herd yesterday.

THE CHAIRMAN: Probably ten.

DR. HENDERSON: O.K. Multiply that by the number of herds.

MR. RUMLER: One and a half per year.

DR. HENDERSON: And then add to that the number of cows, for which we have records--over a million. So you add these and that is the size of the coefficient matrix that we are dealing with. That is why I say that if

you have a computer with unlimited memory and speed, we would store this in the memory and obtain a solution. This, of course, gets completely out of hand, so we look for short cuts, and the obvious one, as Dr. Harvey pointed out, is to use absorption techniques. All of the computational procedures described below take advantage of any possibility of absorbing effects as the data are read.

I have suggested then as an operational procedure that the data be sorted by breeds, herds, sires, cows, and year fresh. I have assumed that a cow has only one record in a given year, but it is not too difficult to relax this restriction.

If we are going to look for the group in which a particular dam is a member, one would have to store the entire data for a herd in memory, and by doing a table search, pair daughters and dams. One had probably better accomplish this on a first pass of the data, at the same time editing the data for obvious errors and writing a new set of tapes which you then used on a second pass.

Then the procedure would involve storing in memory the coefficients and right hand sides for years, the season-ages, dam groups, natural service sire groups, and A.I. sires. Now you will notice that the A.I. sire group coefficients and right hand sides do not appear at this stage, but are computed after all data are read. A very important trick to note is that you do not have to store the entire set of data before you start absorbing. As soon as the data for one cow are read, one can absorb that cow.

The cow coefficients and the right hand side are absorbed into the breed table, and also, depending upon whether the cow is a natural service daughter or an A.I. daughter, are absorbed either into the natural service sire or into the herd.

This suggests a point that I have failed to mention earlier.

We are evaluating natural service sires in this procedure only with respect to a single herd. If a sire is actually used in two or more herds, then one would have to combine, by a tape sort of some kind, your evaluation that you made of him in Herd A, Herd B, and Herd C, and so on. If this were not done, one would have to save in memory all of the N.S. sires, and this would be completely out of the question. It is bad enough with the A.I. sires, 500 to 1,000 of them. You do have to save those because they do get scattered over a lot of herds, and you never know when the last herd has passed through that might have had this sire appearing in it, until the data are all processed.

When all of the data for a natural service sire in a herd are read, one can then absorb the coefficients and the right-hand side for that natural service sire into the herd coefficients and right-hand sides.

At the end of a herd, one absorbs the herd coefficients and the right-hand side. This absorption technique cannot be used readily unless one retains the diagonality of the coefficient sub-matrices. This is the reason for having the herd classified just as a herd effect. If one were to classify by herd-year-seasons, cows will freshen in two or more different year-seasons and the diagonality of the submatrix for herd groups and cows vanishes. I think that we are really forced to regard herds as a separate classification because of this computation problem. In contrast, if one uses only the first record of each cow, she freshens in only particular herd-year-season. If one wants to use that procedure, I would change the model as follows:

Instead of herds, I would have herd-year-seasons, just as we have in our present procedure, and then we could drop years from consideration, because they would be taken care of in the herd-year-seasons. I would still have the season-age classes. And then we would no longer have a classification for cows, and in these absorption techniques involving cows, instead of adding quantities like $(n + \alpha - 1/(n + \alpha)$, we would have $\alpha/(1 + \alpha)$ and $-1/(1 + \alpha)$.

From then on, the computations would be exactly the same way as I have described, except that one would have to redefine the error variance--this would now contain a cow component. Then, after all of the data for a given herd-year-season have been read in, one can absorb since he has not destroyed the diagonality of the sub-matrix coefficients.

At the point where herds are absorbed we add λ if we want to regard herds as random, and we do not add it if we wish to regard herds as fixed. Having absorbed a given herd, we go on then to the next herd and absorb each cow within a given sire, one at a time, and then absorb each natural service sire that comes along in that herd, and then the herd, and just keep on going until we reach the end of the breed.

Well, while doing this, if one wishes to evaluate natural service sires, he would be required, at the end of each natural service sire, to save on tape the right-hand side and coefficients for that sire. At the end of each herd, do the same for the herd.

If we are not going to evaluate natural service sires, we do not have to carry out this operation. So, depending on whether one wants to evaluate natural service sires, he would write out the N.S. sire and herd coefficients and the right-hand side, and later on, having then obtained the estimates of the fixed effects (other than herds) would read these back and estimate the herd effect and then the natural service sire effects.

DR. LEGATES: This is a small point, but suppose you have a lot of the bulls that you have in Class A, and they are not really bulls from your particular area, but these are regional bulls, if you want to think of a random sample from that region, how do you regard these? You see, they are not natural service; you have many herds involved, but you don't want to use them in your estimate for your stud.

DR. HENDERSON: I guess I would call them a separate group.

DR. LEGATES: That's right.

DR. HENDERSON: Yes, the highest grouping of sires.

DR. LEGATES: Lump all of those together.

DR. HENDERSON: Yes, or into several groups. Since the method permits one to take into account the supposed sub-populations from which these animals came.

At the end of a breed one has a set of coefficients and right-hand sides involving Years, SA, DG, NSG, and AIS. We still don't have the AIG coefficients and r.h.s., but we obtain those simply by summing the coefficients and the right-hand side over the A.I. sires of that group.

We then modify the diagonal coefficients of the A.I.S. x A.I.S. part of the matrix by adding σ_e^2 / σ_s^2 . This is the thing that Dr. Harvey was talking about. We then solve the resulting set of equations. Now how many equations would this be? Perhaps 1000. But the greatest part of this comes from the A.I. sires. We still have too big a matrix to store in the memory of most computers, so the strategy of inverting a partitioned matrix might be used in conjunction with disk storage.

Even if we could store the matrix in memory, we would still have a tremendously large set of equations to solve. Whether or not the solution would be accurate would depend upon the word size of the computer being used, and on the nature of the elements of the matrix.

Another possibility is to use an iterative method, particularly with the sire equations. We would first estimate everything except the A.I. sires, by assuming that all A.I. sires estimates = 0. The true solution is in fact the $\hat{\text{AIS}}$ sum to 0 either each AIG. Having obtained this solution one would modify the right-hand sides of the sire equations accordingly and proceed through several iterations.

Having done that, one would correct the right-hand sides for the fixed effects according to the iterative solution to the $\hat{AIS}$ and obtain a new solution to the fixed effects. One would take that solution and readjust the right-hand side of the sire equations, and go through another iterative solution for $\hat{AIS}$, etc.

Before accepting a solution, one should see if the equations are reasonably closely satisfied by the supposed solution.

I should have mentioned that before one starts the solution one must impose four restrictions, one for YS, one for SA, one for DG, and one for AIG (or NSG but not both) if herds are fixed. If herds are random, be sure to impose one less restriction. That is, no restriction is imposed on <u>one</u> of the four sets of effects. This is because adding σ_h^2/σ_e^2 to the diagonals of the herd equations increases the rank of the coefficient matrix by one.

Also, although the true solution is $\Sigma_{\hat{AIS}} = 0$ for each AIG, and this solution would be obtained if word size were large, it is strongly recommended that one force the solution to be this by taking advantage of these identities.

I would suggest that one look at the inverse of the coefficient matrix (ignoring sires).

This inverse does not give the true sampling variance-covariance matrix of the estimators, because it does not take into account sires, but it would probably be a reasonably good approximation to it.

These approximations would give one some idea as to whether the differences that he has estimated really have any meaning.

With respect to the age estimation one probably would plot these and draw a smooth curve to use in practice. These age factors would correspond to the use of regression techniques, and would not be comparable to multiplicative factors. If one doesn't like this idea, he can use the logarithm of the record rather than the actual record in the analysis and thus obtain directly factors that are multiplicative.

This concludes a hasty description of a proposal. If this procedure has any merit, it needs to be tried out. Perhaps this will have to be the Cornell group since we have a large body of data, and hopefully, will have computer time available to do it. If anybody else does have the time and the facilities, I would like to see him try it. I am not too enthusiastic about the

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process of getting the method programmed. The appendix provides some detail in a rather hybrid notation between the usual FORTRAN and statistical conventions.

DISCUSSION

DR. HARVEY: If you made classifications of dam groups by sire groups by herd subclasses, and then had cows nested within these, this would be a straight-forward extension of the procedure that you now use, and you could get rid of allof those equations, couldn't you?

DR. HENDERSON: You could get rid of a lot of those.

DR. HARVEY: You could get rid of the whole set of sire equations there, so why not sacrifice a little of the information and do this?

DR. HENDERSON: Yes, this is a possibility.

DR. HICKMAN: Wouldn't cows' age be in that? Wouldn't that be the first one?

DR. HARVEY: Well, age is cross-classified.

DR. HENDERSON: Yes, age would be cross-classified. This would automatically accomplish the possibly desirable effect of taking into account group-by-group interaction.

DR. HICKMAN: Yes, you would that way.

DR. HENDERSON: Here again one would be faced with larger sampling variances, but possibly less bias.

DR. HICKMAN: We can never get your other procedure carried out.

DR. HENDERSON: There are certainly a lot of ramifications to this model. The technique one would employ is to absorb a set of effects without destroying the diagonality of the sub-matrices and then absorb something else. The more cross-classifications you have, the less one can make use of absorption and the larger will be the resulting set of equations.

DR. TOUCHBERRY: How much precision do you expect to gain by using this procedure, as compared to what is now done?

DR. HENDERSON: I haven't the slightest idea. It depends upon how serious these biases are that we may now have. I think that it would be correct to say that the regions or areas or studs that are doing the best job will probably benefit most by change. The present procedure, for whatever credit I should have for developing it, was based on the assumption, which, I think, was correct at that time, that genetic trends were very negligible. We had pretty good evidence that this was so. And it was based on the assumption that we had a 602-A computer to work with! That wasn't a very powerful computer. And what else? Well, that we had valid age factors, although we weren't so certain about that.

I think that it is pretty clear that many of the assumptions that go into the present procedure are just not valid assumptions any longer, and I think that we are in a precarious situation if we continue indefinitely to use these procedures. The better job we do of selection, the worse the present procedure will get.

DR. TOUCHBERRY: Is it so greatly invalid, if one just compares contemporary sires?

DR. HENDERSON: No. For one thing, age factors don't become much of a problem.

DR. TOUCHBERRY: And, in other words, this is really the bulk of what you want to do anyway, isn't it?

DR. HENDERSON: From the standpoint of bringing sires back into service, yes. However, there is the problem of planned matings to produce sires for future progeny testing.

DR. TOUCHBERRY: But if you are making rapid progress, aren't the sires that you select on the basis of the first proof the ones that you want to pick sons from?

DR. HENDERSON: Yes, if you are really moving fast enough. However, it is conceivable that we might have a freak individual ten years ago that is still better than anything that we now have. For example, look at the Ayrshire Betty Commander bull. Here we have an Ayrshire that is far beyond anything else that we have had in the breed. And now whether or not we will find another one in the population as good as he is is problematical.

DR. MEADOWS: It won't really make any difference because all of the cattle will be his offspring.

DR. HENDERSON: I guess that's right, yes. But we might have a few freaks that might be exceptions, Dr. Touchberry, but I think in general, that what you say is quite true.

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DR. TOUCHBERRY: And, in other words, this is really to [illegible] build of what
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MR. HENDERSON: From the standpoint of primaries since but here
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DR. TOUCHBERRY: But if you are making rapid projections [illegible] the
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DR. TOUCHBERRY: Well, but it is true, and if we do have those freak individuals, I think that we can dig up some freakish way to handle that!

DR. CARTER: Well, if you have followed the differences between ratings of sires on the New York Report and the USDA's report, you will see that there are some sizeable differences on some sires. There are probably many causes, age factors being one of them, but as near as I can tell by what Dr. McDaniel tells me, there are other factors involved that could create quite an error for some of the bulls that are selected and that produce sons for future service.

DR. TOUCHBERRY: Yes, but is the index containing the later records in error, or is the index with the first records in error? If the culling is based on some criteria which indicate that the bull is not genetically sound, then the later records are probably in error, isn't that correct? Now you have a comparison of two indices, but you have not told me which one is in error.

DR. CARTER: No, I am not sure. We have a total group of records. I have a sample out of that total, a sizeable sample, and yet I still have differences.

DR. TOUCHBERRY: I think he is talking about predicting a proof based on later records from a proof based on first records.

DR. PLOWMAN: No, based on different parts of the country.

DR. MEADOWS: Yes, well, the Betty's Commander bull is going to be used right on out, you see, that is the point. A bull that good is going to continue to be used, and Betty has been used as long as he has had semen available.

DR. TOUCHBERRY: Yes.

DR. HENDERSON: Oh, I heartily agree with this, and so in a shorter time period, regardless of whether you use all records, it is just as legitimate, so far as deciding on the use of the bull is concerned. The practical problem is evaluating the new crop of sires. But those who use sire proofs seem to want an evaluation on everything, and it gets a little unpleasant to have a bull with many daughters whose evaluation changes from year to year.

DR. TOUCHBERRY: Do they really want this, or do we think they want this?

DR. HENDERSON: Well, I don't know. This is a good question.

DR. MEADOWS: Is this over a two-year period?

DR. CARTER: They get really concerned when you give then the figures on a sire, and then a year later, you give them a sizeable change in those data.

DR. HENDERSON: We have given the impression that with large numbers we don't get changes.

DR. CARTER: Well, we mean that we don't expect to get proofs that change drastically. For two years, at every meeting that I went to, I knew that before I got out of the meeting somebody would ask, "What is wrong with you people up here that you can't come closer than 800 pounds of milk on a bull?"

DR. HENDERSON: A good question.

DR. GAUNT: What is your answer?

DR. CARTER: Well, I would tell them some of the probable causes of this, but one major one we are connected with is that when you sample a bull and then bring along another crop of daughters with four years between the two groups, you have to consider the genetic trends. Our best estimate in New York right now is about 160 pounds of milk a year--so you have changed your estimate of that bull drastically. We are losing some of the confidence of our dairymen in the figures that we are giving them, when we have such drastic changes.

DR. LEGATES: We need to tell them why this happens.

DR. CARTER: Well, if a sire's proof doesn't change with time then our breeding program is all wrong.

DR. LEGATES: You are supposed to give a proof within a given period of time.

DR. HENDERSON: But the whole point is what are we trying to do with sire evaluation? If what we are trying to do is to compare contemporaries, then a much more simple procedure is what we ought to use. If we are trying to do what people think we are trying to do at the present time, we need something more elaborate.

DR. McGILLIARD: Well, I think that is probably a basic principle that most of them think we are trying to estimate something unique about a bull, and we are not. We are trying to measure the differences between two bulls.

DR. HENDERSON: And two bulls which are contemporaries.

DR. McGILLIARD: Yes.

MR. RUMLER: If that is exactly what you told them, don't fight it, I say.

DR. McGILLIARD: Yes, but they are saying that here is a bull that you estimated 14,000 pounds or so much above, and now this ought to be right and shouldn't change over time.

MR. RUMLER: That is what you told them.

DR. McGILLIARD: No, that is not what we told them. We told them what the difference was between two bulls.

MR. RUMLER: That is different.

DR. HENDERSON: Yes, we think that is different. We think that is clear.

MR. RUMLER: Oh, yes, that's right.

DR. FREEMAN: Yes, Dr. Touchberry has got a point here that was made.

DR. HENDERSON: Yes, I argue with my colleagues about this a good deal. I always prefer to use deviations myself.

THE CHAIRMAN: But the A.I. industry is having difficulty adjusting to the fact that an estimated breeding value, even if it is a deviation, is going to be relative to time, and it is going to change, even though it is based on a very large sample.

DR. FREEMAN: The other thing that hasn't really been made clear is that the purpose is to choose among contemporary bulls.

DR. HENDERSON: Herdmate comparisons, certainly, or contemporary comparisons, if they are contemporary in time, will take care of it; there is no problem there.

DR. MEADOWS: Well, basically we have always talked in terms of absolute values.

DR. HENDERSON: Yes.

DR. MEADOWS: If we started in A.I. we would think in terms of absolute values, but we never do really mean this. What we really mean is one, two, three, four; that is, we try to rank them. So we are always talking in terms of absolute breeding values, and until we get that idea out of our hair, people will always want something absolute. Dr. Touchberry wants something absolute. He wants to know the absolute breeding value for his number one bull. And all that we can possibly ever do is say that this one appears to be better than another.

DR. HARVEY: At this time, and under these conditions!

DR. MEADOWS: At this time, under these conditions, and I don't see the reason for mincing words about it.

DR. CARTER: This means that we could not compare an older progeny tested bull against a young sire whose first proof was just available. So you can't compare those two now, and you are going to have to make your comparisons within some kind of a limited time period.

APPENDIX

Outline of Sire Evaluation Which Accounts For Unknown Genetic and Environmental Trends, Herd Differences, Seasons, Age Effects, and Differential Culling

C. R. Henderson, Cornell University

A. Linear Model

Years	YR	g	fixed
Season-Age	SA	h	fixed
Dam Groups	DG	i	fixed
NS Sire Groups	NSG	j	fixed
AI Sire Groups	AIG	j	fixed
AI Sires	AIS	k	random
Herds	H	p	fixed
NS Sires	NSS	q	random
Cows	C	r	random

B. First Pass of Lactation Records File

1. Sort by breed, herd, sire, cow, yr. fresh. Assume that a cow makes no more than one record in a year.

2. Prepare new data sets with DG recorded. This will require a table search separately for each herd stored in turn in memory.

3. On this pass do any other screening or identification desired.

C. Tables of Coefficients Required to Be Prepared on Second Pass of Data

For the current breed

	YR	SA	DG	NSG	AIS
YR	x	x	x	x	x
SA		x	x	x	x
DG	Not Needed		x	x	x
NSG				x	x
AIS					x

At the end of breed computations, coefficients of AIG are computed from coefficients of AIS.

For the current herd

YR
SA
DG
NSG
each is a vector

For the current NS sire

YR
SA
DG
each is a vector

D. Vectors of Right Hand Sides to Be Prepared on Second Pass

For the current breed

YR,SA,DG,NSG,AIS (and at the end, AIG)

For the current herd

YR,SA,DG

For the current NS sire

YR,SA,DG

Each of the above tables or vectors must be cleared to 0 at the start of a new breed, herd, or NS sire, respectively. Also scalars SUMH and SUMS for herd and NSS respectively.

E. Computations With Individual Records of One Cow

Let n records of a cow be $y_1, \ldots, y_n$ and located in

$g_1, g_2, \ldots, g_n$ yrs $(g_s, s=1,\ldots,n)$

$h_1, h_2, \ldots, h_n$ SA $(h_s \; s=1,\ldots,n)$

Let $\alpha = \sigma_e^2/\sigma_c^2$

Add to Breed Coefficients

YR X YR $\frac{n+\alpha-1}{n+\alpha}$ to $g_s g_s$ cells, $s=1,\ldots,n$

$\frac{-1}{n+\alpha}$ to $g_s g_{s'}$ cells, $s=1,\ldots,n-1$

$s'=s+1,\ldots,n$

$s \neq s'$

YR X SA $\frac{n+\alpha-1}{n+\alpha}$ to $g_s h_s$ cells $s=1,\ldots,n$

$\frac{-1}{n+\alpha}$ to $g_s h_{s'}$ cells $s=1,\ldots,n$

$s'=1,\ldots,n$

$s \neq s'$

YR X DG $\frac{\alpha}{n+\alpha}$ to $g_s i$ cells $s=1,\ldots,n$

YR X AIS (if AI cow) $\frac{\alpha}{n+\alpha}$ to $g_s k$ cells $s=1,\ldots,n$

SA X SA $\frac{n+\alpha-1}{n+\alpha}$ to $h_s h_s$ cells $s=1,\ldots,n$

$\frac{-1}{n+\alpha}$ to $h_s h_{s'}$ cells $s=1,\ldots,n-1$

$s'=s+1,\ldots,n$

$s \neq s'$

SA X DG $\frac{\alpha}{n+\alpha}$ to $h_s i$ cells $s=1,\ldots,n$

SA X AIS (if AI cow) $\frac{\alpha}{n+\alpha}$ to $h_s k$ cells $s=1,\ldots,n$

DG X DG $\frac{n\alpha}{n+\alpha}$ to ii cell

DG X AIS (if AI cow) $\frac{n\alpha}{n+\alpha}$ to ik cell

AIS X AIS (if AI cow) $\frac{n\alpha}{n+\alpha}$ to kk cell

<u>Add to Herd coefficients if AI cow, to NSS coefficients if NS cow</u>

YR $\frac{\alpha}{n+\alpha}$ to g_s cells $s=1,\ldots,n$; AIS $\frac{n\alpha}{n+\alpha}$ to k cell

SA $\frac{\alpha}{n+\alpha}$ to h_s cells $s=1,\ldots,n$

DG $\frac{n\alpha}{n+\alpha}$ to i cell

Add to Breed RHS Vectors

YR $\quad y_{g_s} - \frac{y.}{n+\alpha}$ to g_s cells, $s=1,\ldots,n$

SA $\quad y_{h_s} - \frac{y.}{n+\alpha}$ to h_s cells, $s=1,\ldots,n$

DG $\quad \frac{\alpha y.}{n+\alpha}$ to i cell

AIS (if AI Cow) $\quad \frac{\alpha y.}{n+\alpha}$ to k cell

$y.$ = cow total

Add to Herd RHS if AI cow, to NSS RHS if NS cow

YR $\quad y_{g_s} - \frac{y.}{n+\alpha}$ to g_s cells $\quad s=1,\ldots,n$

SA $\quad y_{h_s} - \frac{y.}{n+\alpha}$ to h_s cells $\quad s=1,\ldots,n$

DG $\quad \frac{y.}{n+\alpha}$ to i cell

Add to SUMH if AI cow, to SUMS if NS Sire

$$\frac{\alpha y.}{n+\alpha}$$

F. Computations at End of NS Sire

This "absorbs" NS sires into other classifications and as a consequence evaluates NS sires only on data for a single herd.

Write NSS vectors and scalar if NS sires are to be evaluated later.

Let $\gamma = \sigma_e^2/\sigma_s^2$

Let C = coefficients of NSS vectors

CS = sum of coefficients in any one of them (all sums are equal)

Subtract From Coefficients in Breed Table

YR X YR	$C_g C_{g'}/(CS+\gamma)$	from gg' cells, $g \leq g'$
YR X SA	$C_g C_h/(CS+\gamma)$	from gh cells
YR X DG	$C_g C_i/(CS+\gamma)$	from gi cells
SA X SA	$C_h C_{h'}/(CS+\gamma)$	from hh' cells $h \leq h'$
SA X DG	$C_h C_i/(CS+\gamma)$	from hi cells
DG X DG	$C_i C_{i'}/(CS+\gamma)$	from ii' cells $i \leq i'$

Add to Coefficients in Breed Tables

YR X NSG	$C_g\ \gamma/(CS+\gamma)$	gj cells over all g's
SA X NSG	$C_h\ \gamma/(CS+\gamma)$	hj cells over all h's
DG X NSG	$C_i\ \gamma/(CS+\gamma)$	ij cells over all i's
NSG X NSG	$CS\gamma/(CS+\gamma)$	jj cell

Add to Herd Vectors

YR	$C_g\ \gamma/(CS+\gamma)$	g cells
SA	$C_h\ \gamma/(CS+\gamma)$	h cells
DG	$C_i\ \gamma/(CS+\gamma)$	i cells

Subtract from Breed RHS

YR C_gSUMS/(CS+γ) g cells

SA C_hSUMS/(CS+γ) h cells

DG C_iSUMS/(CS+γ) i cells

Add to Breed RHS

NSG γSUMS/(CS+γ) j cell

Add to Herd RHS

YR C_gSUMS/(CS+γ) g cells

SA C_hSUMS/(CS+γ h cells

DG C_iSUMS/(CS+γ) i cells

Add SUMS TO SUMH

G. Computations at End of Herd

This "absorbs" herds.

Write Herd vectors and scalars if NS sires are to be evaluated later.

Let D = coefficients of herd vectors

DS = sum of any one of them (all sums are equal)

$\lambda = \sigma_e^2/\sigma_h^2$

Subtract from Breed Coefficients

YR X YR	$D_g D_{g'}/(DS+\lambda)$	gg' cells, $g \leq g'$
YR X SA	$D_g D_h/(DS+\lambda)$	gh cells
YR X DG	$D_g D_i/(DS+\lambda)$	gi cells
YR X NSG	$D_g D_j/(DS+\lambda)$	gj cells
YR X AIS	$D_g D_k/(DS+\lambda)$	gk cells
⋮		
AIS X AIS	$D_k D_{k'}/(DS+\lambda)$	kk' cells $k \leq k'$

Subtract from Breed RHS

YR	D_gSUMH/(DS+λ)	g cells
⋮		⋮
AIS	D_kSUMH/(DS+λ)	k cells

H. Computations at End of Breed

Compute coefficients of

YR X AIG
SA X AIG
DG X AIG
NSG X AIG
AIG X AIG
AIG X AIS

by summing YR X AIS
⋮
AIS X AIS
} Coefficients and r.h.s.

over AI sires of same group

Compute AIS right hand sides by summing AIS right hand sides over sires of same group.

Delete last equation and last unknown of SA,DG,AIG

Add σ_e^2/σ_s^2 to diagonal coefficients of AIS

Solve resulting equations.

Suggested method for solution:

1. Invert submatrix excluding AIS.

2. Solve for all unknowns except AIS from this inverse and corresponding right hand sides. (solution assuming AIS = 0)

3. Assume this is the correct solution and solve for AIS iteratively.

4. Correct r. h. s. of submatrix for current solution to AIS and obtain new solution to unknowns other than AIS.

5. Solve for AIS iteratively.

6. Continue process as many rounds as needed to obtain satisfactory solution.

Precaution: The original inverse should be checked carefully as there could be confounding that would result in singularity or near singularity. In that case more restrictions would be required. One check is to multiply the matrix by its "inverse" to see if the product is not too different from I.

DISCUSSION

THE CHAIRMAN: We will plan to devote the next twenty minutes for a general discussion on any topics that you choose to consider and to use the last few minutes to try to tie together some of these problem areas and define them as well as we can.

DR CARTER: I think that there are two things that we need to establish: Number one is, what changes do we need? What parts of our present program need changing? And the other is: How should we go about doing that? Do we have at present research information available to guide us? Or do we need more?

THE CHAIRMAN: In other words, we have an operational system now. What can we do, research-wise and operationally, to improve it? At the same time, perhaps we can underscore problems which require further research before operational improvements can be made.

MR. RUMLER: I was encouraged by the discussion that has taken place, concerning problems associated with single-herd proofs or non-AI proofs. I wonder whether this is an area in which additional work needs to be done, or whether enough results are available to reach some conclusion here? How should the information for the bull used in a single or limited number of herds be handled?

THE CHAIRMAN: I think that this is a point that very well could be discussed. There were a number of comments made during the course of the meeting that perhaps we should consider the possibility of making further adjustments on the single herd proof. I am not sure whether those who mentioned this were considering the possibility of regressing the unadjusted proof to produce estimated breeding values. I think Mr. Rumler recognizes that we are not nearly as accurate with our tools in evaluating bulls on a single herd basis. However, in an organization such as the Holstein Friesian Association, a large proportion of the breeders contribute heavily to our record keeping program, and hence to our sire and cow evaluation schemes. They may be using AI sires, of course, many of them are. But, none the less, many are also using bulls in a single herd situation. Mr. Rumler frequently reminds me of the fact that approximately seventy-five percent of the bulls summarized by USDA are non-AI bulls. Of course, I like to point out to him that the majority of the daughters are from AI bulls. So, we do have a responsibility, certainly, to do the best job we can with these single herd proofs. The question is now, is there anything that we can do, based on the discussions here, to increase the accuracy of our evaluations? Secondly, might we consider a procedure for these bulls that would result in our producing estimated breeding values?

DR GAUNT: Well, I think that in a way we have been misleading people in the past by the way that we have been listing results in the books; that is, that they could be listed by so many daughters, whereas the AI situation requires more animals. This makes it look as if it didn't take as many to obtain accurate proof, whereas the truth is just the opposite.

I think that this situation needs to be corrected. I also think we should evaluate the bulls in terms of what they might do in another herd because that is what people are thinking about.

If you go about it the other way, let us make it very clear that these are the estimated breeding values of these sires if they are used back in the same herd; this is one of the real dangers, I think.

DR. MEADOWS: Well, Dr. Corley, I think there is a bit of philosophy involved in this question. We have told the AI units, generally speaking, what kind of progeny test design is required for us to come up with a reasonably accurate estimated breeding value to compare their bulls. I think that the breeders also have a responsibility to sample bulls in such a manner that we can obtain an accurate estimated breeding value. I think that we ought to tell them so.

Mr. Rumler and I have had some correspondence on this question; I think my last letter was eleven pages. If he samples more than one bull at a time then I can make an accurate choice among the bulls, but if he doesn't get this idea across, then I think we are lost.

How well we are going to be able to predict what that bull will do across all herds, I don't know. I think that the first step would be for the breeder to sample his bulls in such a manner that he could make accurate choices himself, among those that had been sampled, then there would probably be a market in AI for some of those bulls. But it wouldn't do the AI industry any good to sample one bull at a time. Now as to how well we can assess the progeny test results -- Dr. Henderson said he was going to solve the problem -- I am not sure. There may be an immediate solution, but we may not have that many dollars!

MR. RUMLER: Well, I think we have to face this problem. Here we have what I consider, quite properly, the very best minds that we have in the country. Now we are not just one breed association, but several breed associations saying, all right, what kind of help can you give us? I think this is the first positive step that has come out so far. It is a difficult one, and it would be difficult to even put into effect because there are a lot of problems.

THE CHAIRMAN: What will this procedure do to us in terms of the problem of distribution of herds and daughters? Should one try to devise and develop a scheme for adjusting for distribution of both daughters and numbers of herds?

DR. HARVEY: I don't see any reason why it is not being done right now, myself. Very little extra time and effort would be required. Why assume that every daughter is in a different herd, when you have got computers doing the work? That seems foolish to me. And that is exactly what is being assumed, isn't it?

[illegible] this situation [illegible] to be [illegible] the bulls in [illegible] of what [illegible] what people [illegible] about.

If you go about it the other [illegible] ask it very close that [illegible] the estimated breeding values of [illegible] before it they [illegible] same here. This is one of the [illegible] I think.

DR. [illegible]: Well [illegible], I think there is a bit of philosophy involved in this [illegible]. We have told the [illegible] what kind of [illegible] design is required [illegible] actually accurate estimated breeding values to compare these bulls. [illegible] think that the breeders also have a responsibility to [illegible] in a manner that [illegible] estimated breeding value. I think that we ought [illegible] tell [illegible].

[illegible]: Rumler [illegible] some comments on [illegible] question. I [illegible] my last letter [illegible] pages, [illegible] the samples work [illegible] then I can make [illegible] choice [illegible] bulls, but it [illegible] idea across, then I think we [illegible].

Now well we are going to be able to predict what that bull is [illegible] across all breds, don't [illegible]. I think [illegible] breeder to sample his bulls in such a manner that I could make accurate choices himself, among those that had been sampled, then there would probably be a market in it for some of those bulls. But it would [illegible] the AI industry any good to sample [illegible] at a time. Now as far [illegible] can assess the [illegible] any test results [illegible] be going to solve the problem [illegible] I am [illegible]. [illegible] may not have that many [illegible].

MODER: [illegible], I think [illegible] problem. [illegible] what I [illegible] quite properly [illegible] in the country. [illegible] we are not just [illegible] breed association, but general breed association [illegible] right, what kind [illegible] we have [illegible]? I think this [illegible] the first priority [illegible] that has come out so far. [illegible] it would be difficult to even put into effect [illegible] problems.

MR. [illegible]: [illegible] to our [illegible] breed [illegible] should [illegible] an [illegible]

[illegible] reason why [illegible] in [illegible] and [illegible] adopting the [illegible] and that [illegible] be [illegible]

THE CHAIRMAN: That's right.

DR. HARVEY: You can record the distribution for each sire very easily, and make use of it to more accurately correct for that in the regression coefficient that is being used for AI sires. If it is done correctly, you can drop down to the single herd group and regress them severely; perhaps that is what they need. Perhaps you can come up with a better procedure, similar to what Dr. Henderson has described, but it could even be less complicated!

You might have AI sire progeny in the same herd with the natural proof; then you could get ties that can be used to adjust specifically for these herd differences and not have to use an average adjustment. This would be of tremendous value because the efficiency of comparison would be greater. The regression would still be large, relative to the regression for the other AI sires that are used in a lot of herds, but at least it would be more accurate, I think, if done that way, than it would using σ_H^2 and a denominator divided by one, compared to σ_H^2 divided by ten, fifteen, twenty, or thirty.

THE CHAIRMAN: What is our best information on what this adjustment should be for the single herd proof?

DR. HARVEY: I think that in some work from Cornell they have equations that show just what the composition of that regression factor is involving the herd variance component.

DR. HENDERSON: You automatically regress them back a great deal because of the small numbers involved, however.

DR. HARVEY: Of course, this is all based on the assumption of no differential mating and no preferential treatment.

DR. HENDERSON: That's right.

DR. HARVEY: And now we assume that this is all right, so that we can go ahead and do this. And if we assume that, there is no reason why we can't use this procedure.

DR. HENDERSON: Of course, we are never going to have any real way of knowing in which situation preferential treatment does exist, and in which one it doesn't. So I think that we have got to make up our mind, and we either do it for all sires, realizing that there is this possiblity, or we don't do any of them; I don't know which is the proper decision.

DR. MEADOWS: Well, if you depend upon a comparison between natural daughters and AI daughters within the same herd, I think that you --

CHAIRMAN: That's right.

DR. HARVEY: You can record the distribution for each site very easily, and make use of it to more accurately compute for that in the regression coefficient that is being used for AI sites. If it is done correctly, you can drop down on a dissatisfied head group and increase them accurately. Therefore what I read, Redding, can go with better precision similar to the Northern Hemisphere described but it [illegible] be [illegible]

[illegible] have AI site property in the same bed with the natural group; then you could get rise that can be used to adjust specifically for these bed differences and have to use in a adjustment. This would be of the recommendation, while because the efficiency of comparison would be greater. [illegible] regression would still be large [illegible] to regression for the other AI [illegible] that are used in lot of at least it would be more [illegible] I think, it done that way, that it would [illegible] and a demonstration [illegible] one, compared to of divided by ten. [illegible] or thirty.

THE CHAIRMAN: What is our best information on what this adjustment should be for the single bed group?

DR. HARVEY: I think that in some work from Cornell they have equations that show just what the composition of the regression factor is involving [illegible] variance covariance term.

DR. HENDERSON: You automatically regress them back a great deal because of the small numbers involved, however.

DR. HARVEY: Of course, this is based on the assumption of no [illegible] genetical matting and no preferential [illegible]

DR. HENDERSON: That's right.

DR. HARVEY: And now we [illegible] that this is all right, so that we can go ahead and do this. And if you assume that there is no reason why we [illegible] use this procedure.

DR. HENDERSON: Of course, we are never going to have any real way of knowing in which situation preferential treatment does exist, and in which one it doesn't. So I think that we have got to make up our mind, and we think [illegible] for all sites, realizing that there is this possibility, or we don't [illegible] of them; I don't know which is the proper decision.

[illegible] depend upon comparison between natural [illegible] in the [illegible] here, I think that you --

DR. HENDERSON: Well, I don't know. Under the present circumstances, if there is any differential treatment, it must be in favor of AI, because they are tremendously better. Are you going to change this by changing the sire evaluation procedure? I don't know.

DR. MEADOWS: I was thinking in a single herd situation where a breeder is testing his bull against your bull.

DR. HARVEY: People will still have to look at the individual conditions of such proofs just as they do now.

DR. TOUCHBERRY: It seems to me that regressing the proof gives a much fairer representation of a natural proof versus an artificial one than what is now published.

DR HARVEY: That would be biased the other way.

DR. TOUCHBERRY: Yes, the other way. And it seems to me that there are enough variance estimates of differences between herds, years, and so on that you could get reasonably accurate values. You can get a pretty good approximation, but then you are also trying to get something that is itself an approximation.

DR. HENDERSON: The regression coefficient should be of the form N over N plus something.

DR. FREEMAN: That's right, it should be similar to what I described yesterday with a c^2 term or some similar term -- so that it doesn't tend to 1.0, even with large numbers. And this is easy enough to do, but you may have to guess a bit at what c^2 is.

DR. LEGATES: There are quite a few estimates.

DR. DICKINSON: Isn't the effect of this regression system to bring all of these single herd proofs back very close to the breed average so that, in effect, you are not going to have much spread among the bulls?

DR. HARVEY: If that is the case, then we need to know it.

DR. DICKINSON: If that is so, perhaps we had better spend our time attempting to devise another system of progeny testing that these people using single herd proofs could use instead.

DR. MEADOWS: For example?

DR. DICKINSON: Perhaps distributing the semen from these bulls by some method over, let us say, at least five or six herds. And it would have to be randomly distributed and probably unknown to the breeder if we consider preferential treatment a possible problem, and I consider it very serious.

DR. PLOWMAN: How do you get it done, though?

DR. DICKINSON: We want to do what we can to approximate the AI situation through the random distribution of daughters.

DR. LEGATES: Well, I don't think we are going to do very much to these eleven or twelve thousand bulls, however. You have got these data now, and this is what we are going to have in the next five or so years. There will be more AI herdmates and contemporaries coming into these herds, but essentially a syndicate or working with this kind of thing -- they are going to go to a stud, I believe. But I certainly would favor a regression procedure, and I would be in favor also of determining how many sires are represented. This is the key thing.

DR. MCDANIEL: Not how many herdmates?

DR. LEGATES: You don't have the number of sires?

DR. MCDANIEL: No, we don't have that. In order to do that we would have to redesign our system. We only have cow totals in the herdmate file. We carry the number of cows in that herd month, and the milk, and the fat -- that is all we carry for that herd-month. A distribution of the type that Dr. Freeman is talking about, where you use c^2 is something we can handle. It is very simple. This we can do, but we don't have the procedures for considering number of herdmate sires. In fact, it would require quite a major redesign to do this.

DR. FREEMAN: Well, I suppose that ideally one should use a coefficient here which just automatically took into account the number of herdmates, the number of herdmate sires, and so on, over the complete range from natural service to all AI. There is no reason why this can't be done. And that is what Walt was talking about. But I suppose this would mean considerable reprogramming.

DR. HARVEY: But it wouldn't be very serious; it wouldn't be a very major change, would it?

DR. FREEMAN: I don't think so.

DR. DICKINSON: But it still doesn't get us out of the problem of the natural proofs being regressed close to the breed average, and still gives us very little basis for differentiation.

DR. FREEMAN: I agree with your first statement in principle 100 percent. But to get it accomplished is not something that we are going to do overnight.

DR. DICKINSON: That's right.

DR. YOUNG: Well, essentially this is what ABS does with their EDS, isn't that right? Well, a lot of those EDS's still come out quite a long ways from zero.

[illegible]

[illegible]

[illegible]

DR. BARR: They still consider the dam.

DR. YOUNG: Well, I don't think that usually affects it very much, though.

DR. CARTER: It has some effect.

DR. YOUNG: The herd level does affect it markedly quite often.

DR. MCGILLIARD: I guess I am curious as to what decisions will be made with the proofs, after you compute them, what types of decisions will be made?

DR. YOUNG: Well, I think that some of the breeders probably would use them.

DR. MCGILLIARD: For what?

DR. YOUNG: To make decisions on which natural-proof bull they want to use.

DR. MCGILLIARD: So it doesn't matter then in what form they are. They are O.K. like they are for all practical purposes.

DR. YOUNG: Well, they are not as easily compared though.

DR. LEGATES: Even for that, adjustment for number of daughters would be helpful.

DR. MCGILLIARD: And I suppose the other decision to be made is whether they use an AI sire or use their own bull.

DR. LEGATES: Which would help them.

DR. MCGILLIARD: Well, I don't think it would help them at all.

DR. YOUNG: Well, I would agree with Dr. Meadows. I think that the first thing to do is for the breed association to try to educate the breeder that it is necessary for the bull to be proven as accurately as possible. If he can't be placed in an AI stud situation, then if possible he should be used in several commercial herds. If this can be done for a number of years, it should be possible to accurately assess a proof made in this way. In the meantime, I suppose you have to do the best you can using something like Dr. Harvey has suggested.

DR. SMITH: Well, if a breeder is interested in getting an accurate proof on his bull and does pass semen around to several herds these sires will be regressed using c^2 factor or something according to the number of herds. So as you approach the situation where a breeder actually gets his bull sampled in more and more herds, he will get more and more advantage of the regression and nearly approach AI conditions; this would be an encouraging factor.

If a breeder is only going to prove his bull in his herd, and perhaps gives preferential treatment, there is nothing that you can do to evaluate his situation. But even if he carries out a reasonable progeny test within his own herd, he gets a stiff regression to the mean because it is only one herd. If he goes to two herds, he gets a little better break. And if he goes to four or five or six, well, then he begins to get a more accurate proof. And this we take into account in the computation of the number of herds, even if you couldn't use the distribution of the number of sires that he was proved next to, which is really the trouble, the number of sires he has daughters standing contemporarily with.

THE CHAIRMAN: This is changing the subject, but I would like to raise a question to Dr. Van Vleck concerning the material that he presented regarding making use of records in progress as well as complete lactations as a package scheme for sire evaluation. I believe that you implied that problems involved in implementation, in implementing this, were largely operational. I can understand this. Are there research questions that need to be answered?

DR. VAN VLECK: Well, I think that the research needs are pretty well illustrated in the handout or what I gave. I don't think that there is any real problem of research in that area if we follow that general type of procedure.

THE CHAIRMAN: Well, I presume, Dr. McGilliard, that this is not necessarily the case when one looks at the problems that we have now in projecting records, with the existing factors. I would suspect that you could suggest some areas of research that are needed here to improve upon the present practice for projecting records.

DR. HENDERSON: Well, that is what you were implying too wasn't it, Dr. Van Vleck, that you just need better estimates?

DR. VAN VLECK: Yes.

DR. HENDERSON: But no one estimate at this point of parameters is needed, but it is a question of getting better estimates of the parameters we know about, and we just need a little more data. I hope that is what Dr. McGilliard and Dr. Van Vleck both indicated, I am not sure.

DR. MCGILLIARD: Well, there is another problem in the whole thing, or there may be two more problems:

One is this circularity which I have heard mentioned, I think, in every paper in which we have something that we would like to measure; we don't know what it is. We have a couple of measures of this thing, and we would like to choose the one which measures it the best. We don't know what we are measuring so we have to choose a measure to match our measures against, and we just go around and around and around. Now this is a real difficulty. I think that a good analogy is one that my son brought to my attention last

week. In one of the camera magazines there was a comparison of color film -- Ectachrome, Kodacolor, and this sort of thing. And the thing that was done was to take a picture of a colorful scene, and a couple of pictures were filmed and then sets of these for each type of film, and then you were asked to choose the one that portrayed most closely the actual colors as probably the film that you would like to use. Well, you could check to see whether one film takes the colors the same way from one time to another. You can compare between the films and choose the one that you think is the most colorful and most resembles the original scene. But I will be darned if you can choose the one that resembles the original scene because you didn't see that! I think that this is what most of our procedures do. We develop a couple of procedures and we match them, and we say, well, this one looks better to us, and it probably measures what I want to measure, but whether it does or not, we don't know. And with the part records you could get actual production for the whole lactation for any part of this sort of thing so you do have something to match against which could be measured, actually, if you want to get it down to the tedious job of measuring a lot of these complete lactations.

But then other problems come up. Now we have measured this complete record at one time, and then we have developed a procedure which samples this pretty well and estimates pretty close to what the actual is, and so we said, O.K.; here is an easier way, and we will take this and it has done a pretty good job. And pretty soon we get a little tired of this, and we pick up another measure, and we say now we will match it with our first measure -- not with the actual, but with the first measure. And we say, well, this measures this pretty well; let us adopt this one.

And about six steps on down the road we don't have any idea whether this one measures the actual closely at all. It measures the one just before pretty well. So here is another problem even where we do have something to match.

DR. HICKMAN: I think there is another question. I think there is another one that has to be taken into account in estimating these extension factors, and that is the different kinds of herd management.

It seems to me that nowadays we are getting more and more herds of cows that never go on grass. In other words, they are fed indoors year round, this feed stall idea, compared to the more traditional method.

Now is there a difference here that hasn't been taken into account yet or should be taken into account? In other words, I would imagine that in the herds that are fed indoors year round there is a different yield -- season relationship -- so that short records versus long records, the relationship between the two might be different, and it would seem to me a new situation over the more traditional method of managing cows.

[illegible] of this sort of thing. And the thing that was done was to take pictures of a colorful scope, and a couple of pictures were taken and [illegible] seen of these for each type of film, and then you were able to choose the one that portrayed most closely the actual colors as [illegible] the film that you would like to use. Well, you could check to see [illegible] one film takes the pictures the same way from one time to another. You can compare by the [illegible] and choose the one that you think is the most colorful and most resembles the original scene. But I will be damned if you can choose the one that resembles the original scene because you don't [illegible] that. I think that this is what most of our procedures do. We develop a [illegible] of procedures and we match them, and we say, well, this one looks [illegible] to [illegible] and [illegible] probably measures what I want to measure, but [illegible] it does [illegible] we don't know. [illegible] with the past records you could [illegible] position for the whole location for any part of this sort of thing so you [illegible] suggesting to [illegible] against which [illegible] measured, actually, if you [illegible] to get [illegible] down to the bottom job of measuring a lot of things [illegible]

But then other problems come up. [illegible] we have [illegible] this complete record [illegible] then we have developed [illegible] procedure which supplies this [illegible] well and [illegible] pretty close to what the actual is and we said, O.K., here is an analog way, and [illegible] will take this [illegible] done [illegible] pretty good job. And pretty soon [illegible] get a little tired of this and [illegible] pick [illegible] another measure, and we say now we will match it with [illegible] first measure -- not with the actual, but [illegible] we first [illegible] And [illegible] say, [illegible] this measures this [illegible] Let us adopt [illegible]

And about six years on down [illegible] and we don't know [illegible] tion whether this [illegible] measures the actual closely at [illegible] it measures the one just before [illegible] well. So here is another [illegible] we do have something [illegible]

DR. HIGGINS: I think there is [illegible] I think there is another [illegible] be taken into [illegible] estimating [illegible] factors [illegible] that is the different alone [illegible] herd management.

It seems to me that nowadays we are getting more and more needs of [illegible] we've go on guess. In [illegible] words, they [illegible] industry wants [illegible] all idea, compared to the more traditional method.

[illegible] a difference here that hasn't been taken into account [illegible] taken [illegible] account? In other words, I would imagine that [illegible] to [illegible] years ago when there is a different [illegible] that they [illegible] to long records, the [illegible] can not be [illegible] and it would seem to me [illegible] are of [illegible] local method [illegible] managing cows.

DR. MCGILLIARD: Now the only thing that I can say about this is that the comparison has not been made precisely. But when the difference was between herds and an attempt was made to measure these, in general, the difference was small, and this is not to say that you can't separate out a certain group.

DR. GAUNT: This says that the difference wouldn't be big.

DR. MCGILLIARD: That's right.

THE CHAIRMAN: Are we in agreement that if we took the short-term aspects of our program, that we really need separate sets of projection factors? Exactly how these are to be derived, I am not sure that I am in a position to say. But we do, at least, need separate sets of projection factors to apply to these different conditions, records in progress, and terminal records.

DR. MCGILLIARD: I would say so, but I think before we worry a lot about this that we probably should decide between Dr. Van Vleck's suggested procedure and some alternatives which would use projection factors. If we are going to go to his, I guess we should forget about the projection factors.

THE CHAIRMAN: Are there compromises that one might consider short of Dr. Van Vleck's proposal? We recognize that this is a kind of goal to look forward to. I think that the question was raised yesterday as to whether or not one might consider the use of a lactation record shorter than 305 days. Perhaps 150 days or 180 days or what have you.

DR. YOUNG: Ninety days?

THE CHAIRMAN: This, of course, would introduce a completely new set of problems, as we look at the total program, certainly. But from a research point of view, do we need to be concerned about the possibility of using a shorter record than a 305 day record?

DR. HENDERSON: Is this cutting them off at a certain shorter period or taking whatever length they were at the time that the evaluation was done up to and including 305 days?

You see, this cow had 50 days; this cow has 180; this cows had 240 -- and use whatever they have and project it to 305 and use those. Was this the proposal that was made yesterday?

DR. MCGILLIARD: That is what I suggested.

DR. HENDERSON: That is what I gathered. This would probably be somewhat easier, although I don't know -- Dr. Van Vleck's idea could be incorporated also.

DR. [illegible]: Was the only thing that I can say about this is that [illegible] and not [illegible] probably, [illegible] was known [illegible] and in attempt was made to measure these, [illegible] difference [illegible] and this is not to see that [illegible] out [illegible]

DR. [illegible]: This says that the difference would [illegible] big.

THE CHAIRMAN: Are we in agreement that if we took the short-term [illegible] of our program, that we really had [illegible] projection [illegible]? Exactly how these [illegible] be [illegible] I am not sure that I or in a [illegible] say: But we do [illegible] separate sets of projection [illegible] factors [illegible] apply to these different [illegible], records in progress, and [illegible]

DR. [illegible]: I would say so, but I think before [illegible] worry a lot about this [illegible] we probably should [illegible] between Dr. Van [illegible] and [illegible] pro-[illegible] and [illegible] would [illegible] projections. If we are going to [illegible] really [illegible] about the projection [illegible]

THE CHAIRMAN: Are there compromises that one might consider short of Dr. Van Vleck's [illegible] recognize that this is a time of gain to look forward [illegible] I think that the question [illegible] raised yesterday as to whether [illegible] not [illegible] might consider [illegible] of [illegible] for [illegible] than 365 days. Putting 450 days [illegible] have your [illegible]

Dr. [illegible]: Ninety days?

THE CHAIRMAN: This, of course, would introduce a completely new [illegible] of problems, as we look at the [illegible] program, [illegible] but from research point [illegible] we [illegible] recommended [illegible] feasibility of doing a shorter record [illegible] recently?

DR. HENDERSON: Is this cutting them off at a certain shorter period or taking whatever lactation [illegible] which the evaluation was done [illegible] days?

See, this cow had 50 days; this cow has 240 -- [illegible] distance they have the project [illegible] and use those. Was this the proposal [illegible] was [illegible] last year?

[illegible] what I suggested.

What I gathered. This would probably be [illegible] could be

DR. VAN VLECK: Well, just one comment: I don't think that there is really too much difference between the two methods because the problems involved are going to be much the same. You are going to have problems with extension factors, you are going to have problems with variance components, and it is just the same way, so it is really the same problem. It is just a different way of looking at it.

DR. HENDERSON: As far as I can see, they involve the same parameters.

DR. YOUNG: Would it be feasible to punch out a 150-day record on each cow, as is done with the 305-day record now?

DR. HENDERSON: Well, we did it one time on the 650. Was it 150 or 180?

THE CHAIRMAN: I would certainly say that it would be feasible. There would have to be some reason for it, and it would take a lot of convincing to get it done.

DR. MCGILLIARD: I guess that the thing that I would object to most in this sort of thing is that I see as very likely the prospect of what I call "shotgun testing", where the tester goes on the farm maybe twice or three times a year and samples. And then I think, operationally, it is much simpler with the projection factors to kick it to whatever basis you want.

DR. DICKINSON: Do you think that would be acceptable as a management tool by dairymen, or simply for our purpose of trying to get more information on sires?

DR. MCGILLIARD: Well, I think so.

THE CHAIRMAN: Dr. Van Vleck, did you indicate yesterday that you were going to explore further the use of this scheme that you propose?

DR. VAN VLECK: Well, this is generally what we were planning to look at. I don't think that it would interfere with the shotgun testing scheme at all because the same procedures work pretty well for that. I don't really think that we are talking about two different things at all. It might look different from just looking at a 305 against say a 30-day record, but we are extending most of them. And you have to have the same parameters to adjust them somewhere along the line.

DR. FREEMAN: Just the same thing then in different directions.

THE CHAIRMAN: Another item that we might want to kick around a bit further would be this question of age conversion factors.

MR. VAN [illegible]: Well, that's one way. I don't think that's really too much difference [illegible] the two methods because [illegible] are going to be much the same. You are going to have problems with [illegible] in your [illegible] and have problems with variance components and it is just the same way, so it is really the same problem. It is just a different way of looking at it.

DR. HENDERSON: As far as I can see, they involve the same parameters.

DR. YOUNG: Would it be feasible to punch out a 150-day record on each cow, as is done with the 305-day record now?

MR. HENDERSON: Well, we did [illegible] one time on the cows. Was it 150 [illegible]

THE [illegible]: I would certainly say that it would be feasible. There would have [illegible] reason for it, and it would take a lot of convincing to do it [illegible].

DR. [illegible]: I guess that the thing [illegible] would object to [illegible] in this sort of thing is that we are very [illegible] of what I call "shopping testing", where the tester goes on the farm [illegible] and [illegible] times, [illegible] and samples. And then I think, operationally, it is much simpler with the projection factors to kick it to [illegible] where you want.

MR. DICK: Do you think that would be acceptable as a management tool by farmers, or simply for our purpose of trying to get more information on [illegible]?

MR. WILLIAMS: Well, [illegible]

THE CHAIRMAN: [illegible] I'd you had come yesterday that you were going to explore further the use of this scheme that you [illegible]

MR. VAN [illegible]: This is particularly what we were [illegible] to look at. I don't think that it would interfere with the [illegible] testing scheme at all because the [illegible] procedures work pretty well for that. We don't really think that we are [illegible] about two different things at [illegible]. It will look different from just looking at a 305 against say a 30-day record, [illegible] are extrapolating [illegible] and you have to have the same parameters [illegible] adjust them somewhere along the line.

[illegible] Just the same thing then in different [illegible].

[illegible] that we might want to look around a bit [illegible]

DR. MEADOWS: Before you leave the projection factors, you don't really know what influence that your incomplete terminal records have on the balance. It looks to me like you ought to make this decision. If someone wants something to do, this can be done. Do you agree with this?

DR. MCGILLIARD: Well, I agree partly, and I disagree partly. I say you do look at it, and it doesn't change it, and everything is all right you know what it is, but if you do look at it and it does change it, which one do you choose?

DR. MEADOWS: Well! You have got to come to that!

THE CHAIRMAN: I believe the view was very strongly expressed that we would be advised to weight records at the present time according to length. Am I correct in this as being a kind of consensus?

DR. FREEMAN: Weighted according to length how?

THE CHAIRMAN: According to the number of days.

DR. HARVEY: According to the correlation.

DR. FREEMAN: You mean if you went to using incomplete records? I am just asking for a clarification of your question here.

THE CHAIRMAN: Well, my question is whether or not there was a concensus as to the desirability of our weighing records going into our system according to days in milk?

DR. MCGILLIARD: They do use the incomplete records, don't they?

THE CHAIRMAN: Yes, incomplete records are used.

DR. FREEMAN: On this segment of them?

THE CHAIRMAN: On this segment, yes; certainly not complete records. This, apparently, is a fairly easy scheme, and if I am not mistaken, Dr. McDaniel, as a part of our converted procedure --

DR. MCDANIEL: No, not all the way. You have got to weight the herd mates too. As we are set up now we don't have the weights for the herdmates. We can get these weights by using parameters. There are a few estimates based on a relatively small number of observations. I think that it goes back to the same problem that Dr. Van Vleck has mentioned. We can't really weight these until we get some better parameters because the only two basic estimates in American literature that I know of are those of heritability of dams and again those are relatively small numbers of observations.

DR. HENDERSON: Well, I think that at the same time there ought to be a weighting for the record that each cow has. This is such a minor change that if one is going to go part way you should go all the way on that one.

DR. LEGATES: And this is the whole distribution from one test to many tests.

THE CHAIRMAN: Any other comments on this area? Dr. Van Vleck?

DR. VAN VLECK: I would like to go back to the first question that we have talked about, and I wonder if it is necessary to compute the natural service proofs four times a year, or whether it is necessary to publish them at the same time and in the same book as the AI proofs?

DR. DICKINSON: Could you tell us how much of a change occurs on the average in these natural proofs?

THE CHAIRMAN: I can't, but you could figure it out based on numbers, at least, theoretically.

MR. BALDWIN: Natural proofs jump around quite a bit.

DR. GAUNT: I would like to see them grouped and, in other words, obviously, if you publish the AI's together and the naturals together it would be quite a help.

DR. BARR: I would like to see this done, Dr. Corley, for maybe a little different reason. If nothing else, immediately, you point out a lot of the unique problems that exist in proofs that really can't be seen too well the way the data are distributed in the book -- I mean, in the AI proofs.

As for myself, as I go through that book, I know that I am giving weight zero to single-herd proofs because I just won't look at them. But let's face it, we don't publish them in our State for circulation to dairymen so if it doesn't do anything more than this, it will point out the kind of problems that do happen operationally. There is a lot of difference between what happens operationally and what happens when we take a big body of information at one time. And then this might point out the kinds of regressions that might work more satisfactorily operationally than others. And besides, the c^2 might be used.

DR. FAIRCHILD: I think that this is a good point, and I feel that we get two uses:

People who don't have much faith in the natural service proof, when we get this thing, tend not to look at it at all. And yet, on the other hand, when you take it out to a dairyman as they are published now he goes to the other extreme, and he just doesn't know what this particular difference is or he has only a vague idea, and he looks at a herdmate difference on an AI and a herdmate difference on a non-AI as being comparable.

So you have got one person there. And I think that it is just good education to bring these two things together on a comparable basis.

If you list them separately, you should use, as Dr. Gaunt suggested, not a regression that is going to tell them what they do in that same herd, but what they are going to do in an AI population.

DR. FREEMAN: Dr. Corley, you asked for comments, and I think I said the same thing yesterday. I would publish the non-AI proofs using weighted regression factors, as someone said here, and I would publish them in separate lists.

DR. PLOWMAN: Would you compute a predicted breeding value on these?

DR. FREEMAN: Using some sort of environmental correlation value, yes.

DR. PLOWMAN: I think the problem is similar to the situation at ABS. They are doing a similar sort of thing, and they still come up with bulls that are plus six, seven, and eight hundred pounds of milk superiority. Now, if you label this a predicted difference, and you come up with six or seven or eight hundred pounds superiority, are we willing to say that this is what these bulls are going to do in AI? And if we print them and put them in a book, isn't that the interpretation that is going to be put on them? And if this is so, I think that they are going to get a tremendous amount of attention.

DR. MCDANIEL: Could I raise a question on this now? It seems to me that what we need to do is to regress them for predicted breeding value, as has been proposed here, but when we do this, that we stick beside this proof the regression, expressed as a percentage, and when we take one of these bulls that is 4,000 pounds on five daughters and regress him perhaps he comes back to 500 pounds, but we print a five percent accuracy figure beside the proof.

And then we not only express the fact that this is the unexpected mean value of a group of bulls, but we will say, by this accuracy figure, that this on the average has a much wider confidence interval than some AI proof of plus 500 pounds. And isn't this the way to handle it?

THE CHAIRMAN: This point was discussed, by me at least, out at the NAAB meetings in Denver. Really, we came into this discussion in a roundabout way in talking about what minimum level of number of comparisons we should use. As you know, we have always used five. And this does seem to be a ridiculous level from many standpoints, but from another standpoint you have got to start some place. And in the colored breeds you don't get as much information, especially on the single herd proof. Why have it different from one system to another?

Would the artificial breeding industry be receptive to attaching to the AI proof a confidence statement, an arithmetic expression, of this ratio? We took a straw vote, and they were all in favor of it. So I don't know how much help this will be, but it is something that apparently the AI industry would be interested in.

DR. CARTER: I think that it is needed in the AI industry. I have worked with the sire committees in New York for a long time, and I have had a terrible time trying to get across the fact that the superiority that you need on a bull with twenty daughters isn't the same that you need when you have got a hundred daughters; that you regress more and your standard deviation is greater. And this has been a very difficult thing to get across. I think that if they keep seeing this in print and following bulls that this is one of the things that will help us in this educational process.

DR. HICKMAN: Of course, this brings up another question as to whether the daughters of the bulls that you are comparing are contemporary or not. If you have, say, a thousand daughters per bull, but seven hundred of them are six years previous to the daughters who are now being compared with most of the bulls that you are interested in then I don't think the standard formula would apply.

DR. CARTER: Well, even the point estimated would apply.

DR. HICKMAN: I think we should omit the daughters that aren't contemporary and use only the daughters that are of primary interest; then I think that the standard procedures would apply.

DR. HENDERSON: I think we can get unbiased point estimates and put unbiased point estimates on them.

DR. HICKMAN: That's right.

DR. HENDERSON: With the reservation that you are talking about by putting a suitable c^2 value in the regression, we might have a situation in which all of the bulls that are in fact +700 would have natural service estimates that would average +700. They would vary more above that than the +700 average bulls in AI -- with AI very much less. The procedures used ought to point this out to the users of the information.

[illegible] meetings [illegible] Really, we came [illegible] about way in talking about [illegible] should use. As you know, we have [illegible] a ridiculous [illegible] for [illegible] have got to start some [illegible] And in [illegible] much information, [illegible] have it [illegible] from one system to another.

Would the artificial [illegible] AI proof a confidence statement [illegible] radio? We took a [illegible] know how much help this [illegible] it is [illegible] that [illegible] AI [illegible] would be [illegible]

DR. CARTER: I think the [illegible] is needed in the [illegible] worked with the size [illegible] in New York for [illegible] a terrible time trying to get across the fact that [illegible] need on [illegible] bull with twenty daughters isn't the same [illegible] have got a hundred daughters that you [illegible] more [illegible] deviat[illegible] is greater. [illegible] has been a very [illegible] across. I think that [illegible] bulls that [illegible] of the things that will [illegible] proceeds.

DR. [illegible] course, this bridge or another [illegible] whether the [illegible] of the bulls that [illegible] are comparing [illegible] or not. If you have, say, a thousand daughters [illegible] of them [illegible] six years previously [illegible] the daughters who [illegible] with [illegible] of the bulls that [illegible] are interested [illegible] standard form [illegible] would apply.

DR. CARTER: Will [illegible] point [illegible] would [illegible]

DR. HICKMAN: I think we should [illegible] daughters that are [illegible] contemporary [illegible] use only the daughters [illegible] are of [illegible] interest [illegible] then I think that the standard procedure would apply.

DR. HENDERSON: I think [illegible] can [illegible] unbiased point [illegible] and [illegible] multiplied [illegible] matter [illegible]

DR. HICKMAN: That [illegible]

[illegible] the reservation [illegible] you are [illegible] about by [illegible] alive in the [illegible] we might [illegible] [illegible] multiplied [illegible] [illegible] one [illegible]

DR. FREEMAN: I want to raise a point with Dr. McDaniel here, some way or other, because to me this has some problems in it. I don't know what you mean by the term accuracy, but if you use the square root of the regression factor, what you have really done is to regress this back once with the regression factor and, supposedly, the probability that your estimate is above or below the true estimate should be equal.

DR. PLOWMAN: Yes, you have already taken this into account.

DR. CARTER: This is the assumption, but this is not true.

DR. MCGILLIARD: And then you see, I still don't believe this.

DR. TOUCHBERRY: You regress it back for the predicted value, and then you say that that has a wide limit on it.

DR. MCGILLIARD: That's right.

DR. TOUCHBERRY: The true value may be way up or way down from your estimate. And then you say, I will be conservative with him, and I will take him down some more. I don't believe that.

DR. HENDERSON: You might want to choose one of these with a large confidence level because the probability is pretty high.

DR. STARKEY: While we have this group together, is there any merit in taking a straw vote, shall we say, on how many think that publishing these separately would have some practical advantage? I have heard different views expressed.

DR. TOUCHBERRY: Before you do that, I have heard it advocated to publish them separately, and I guess there are one or two reasons for publishing them separately, and there are reasons why they should not be. What are you going to gain? If you regress them and publish them together with this confidence value with them, it seems to me that this would do more to point out the expected error than publishing them separately.

DR. STARKEY: I think just the ease of using the book would be my first point. And in other words, from an extension standpoint, if I want to find a bull, I don't want to look through one large list. And then the next step, of course, would be to just put them in a little separate publication then.

DR. TOUCHBERRY: Now if you put them in a separate publication, you are attaching a stigma to one or the other right away.

DR. STARKEY: Well, I assume that is what we have all been doing for two days here, haven't we?

[illegible] not go [illegible] a point with [illegible] Mathematical here, some [illegible] to me this [illegible] some problems in it. [illegible] don't know [illegible] the term accuracy, but if you use the square root [illegible] [illegible] you have [illegible] done is to express this back [illegible] [illegible] and, supposedly, the probability that your estimate is above or below the true estimate should [illegible] equal.

DR. PLUMMAN: Yes, you have already [illegible] this into account.

DR. LANTER: This is the assumption, but this is not true.

[illegible]: And then you see I still don't believe this.

VONHERNDY: You express [illegible] back for the predicted value, and then you say that that has [illegible] limit on it.

DR. GILLIAMSON: That [illegible]

DR. VONHERNDY: The true [illegible] may be way up or way down from your estimate, [illegible] then you say, I will be conservative with him, and I will take [illegible] on some more. I don't believe that.

DR. HENDERSON: You might want to choose one of those with a [illegible] because the probability [illegible] pretty high.

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DR. [illegible]: Before you do that, I have heard it advocated so publishing them separately, and I guess there are one or two reasons for publishing them separately, and there are reasons why they should not be. What are you going to point? If you express them and publish them together with quite considerable value [illegible] them, it seems to me that this would do more to point out the expected error than publishing [illegible]

DR. [illegible]: I think just the case of doing [illegible] would be [illegible] point. And in other words, [illegible] expression standpoint, it I want to find [illegible] [illegible] one large Iliff, and then the [illegible] [illegible] put them [illegible] separate publication [illegible]

[illegible] them in a separate publication [illegible] other it be away.

[illegible] what we have all been doing.

DR. TOUCHBERRY: Perhaps justifiably or unjustifiably.

MR. BALDWIN: I want to say that the AI industry in general feels very strongly that the designation of AI sires be kept separate.

DR. STARKEY: Designation?

MR. BALDWIN: Designation.

DR. GAUNT: Would you rather have them separated? Our assumption is that this estimate is not biased. These questions are involved in the economic return of the sale of a bull. I think there is a bias here, and this has certainly been shown time and time again; we should try to get the sire's proof in an AI situation -- in other words, I think that there is another reason for keeping these proofs separate.

If you put them together, people just will not distinguish between them, and I don't think that this accuracy value goes quite far enough. I don't know how you could evaluate it properly, so I would say list them separately.

THE CHAIRMAN: I believe the paramount question in this matter of whether they should be separate or not would be whether or not we would estimate breeding values on single herd proofs.

In other words, one might have to look at this two ways depending on whether we continue the present procedure or estimate breeding values of non-AI sires. Should we separate the two groups?

DR. STARKEY: I guess, to me, it wouldn't make any difference. In either case, I think that you have justification for looking at them separately. I think that the person looking in there for a sire would tend to be looking for either one that is available in AI or a natural bull that they might want to buy.

THE CHAIRMAN: I think that age conversion factors were pointed out as being a real shortcoming to our program. I don't mean that I just learned this today, but I don't think that I was as aware of the importance of this problem back through the years as, perhaps, I should have been. Dr. McDaniel has suggested them in terms of these short-term approaches, the use of regionalized factors. I think that we would appreciate any comments that you would have as to whether to make use of these or not at the present time. We have assumed that they are better than what we have been using, and we have assumed that they are not as good as possible, certainly, but that, in view of this, we would probably be advised to proceed to use them as soon as possible. Would you agree to this?

DR. CARTER: Absolutely.

DR. GAUNT: Right.

DR. TOCHEMEYER: Perhaps [illegible] overall [illegible]?

MR. BALDWIN: I want to say [illegible] very strongly that the [illegible] AI prices be [illegible].

DR. STARKEY: Designation?

MR. BALDWIN: Designation.

DR. CAUDT: Would [illegible] rather [illegible] thus this estimate is not biased. These [illegible] economic return of the [illegible] bulk. I think [illegible] was certainly [illegible] shown time and time [illegible] proof in [illegible] AI situation [illegible] reason for [illegible] these [illegible].

If you put them together, people just [illegible] them, and [illegible] I don't [illegible] how you [illegible] evaluate [illegible] separately.

THE CHAIRMAN: I believe [illegible] whether they should be separate or [illegible] would be [illegible] estimate [illegible].

In other words, one might [illegible] on whether we continue the present [illegible] of [illegible] Should we separate the two [illegible]?

DR. STARKEY: I guess, to me, it would [illegible] either case; I think [illegible] separately. I think [illegible] to be looking for either one that is [illegible] they [illegible] to day.

THE CHAIRMAN: I think that age [illegible] factors were [illegible] being a real [illegible] coming to our program. I don't [illegible] this [illegible] but I don't think that [illegible] problem [illegible] has [illegible] regional factors. I think that [illegible] would appreciate any [illegible] you would have as to whether to make use of these or not at this [illegible] We have assumed that [illegible] are better than [illegible] have assumed that they are not as good as possible [illegible], but in view of this, I would probably be [illegible] as possible. Would you agree to [illegible]

MR. ARTER: Absolutely.

DR. HENDERSON: I thought you were using them until Dr. McDaniel told us you weren't.

THE CHAIRMAN: Well, as of today.

DR. HICKMAN: Different factors by seasons?

THE CHAIRMAN: The only problem that we have operationally is that questions come up on, "Why did my State get pooled in with this other State", you know, so we would have to live with this kind of a problem. But there are some objections to this, and justifiably so, I think.

DR. BURNSIDE: There is one point here that I think might be worth making: That is the fact that if one starts to use a number of these correction factors and at any time looks at individual records, M. E. records, either averages or particularly individual records of cows, which I am sure your breeders do presently use, you are going to increase regional and seasonal differences because these factors do magnify any seasonal and regional difference. The procedure that I have recommended for use in Canada uses separate age curves for different seasons and compares the actual records to the average of all cows of that particular age and expresses it as a percentage getting away from actually reducing the gross seasonal effects. I think that there is a definite advantage to this approach any time that one goes to additional factors and looks at actual records or ME records afterwards.

THE CHAIRMAN: I think that once we use these factors, we will need to really ascertain to what extent they have helped us, hopefully, quite a bit, but we will have to find this out.

DR. MCDANIEL: Well, the objection that Dr. Burnside has here is very valid. There is no question at all that the usefulness of an ME record, a herd average or anything else is impaired to some extent because the system we have now tends to level out the seasonal effects and their regional fluctuations. This is true. These were designed primarily for use in getting deviations from herdmates, and this is the way that they were designed primarily for this purpose.

DR. BURNSIDE: This multiplication does it, and if you go the other way, then you will knock it out.

DR. SMITH: Well, in going the other way, wouldn't it be more practical if we would convert our age to, say, twenty-seven months or thirty months, and this way we would be multiplying by factors less than one. And we would, at least, not be inflating the differences when we made our conversions. We would use a factor that ranged from .85 to 1.0 instead of 1.0 to 1.35 or something.

DR. [illegible]: Thought you were going then [illegible] us you [illegible]

THE [illegible]: Well, it's 6 o'clock.

DR. [illegible]: Different factors by seasons?

THE CHAIRMAN: The only problem that we have [illegible] questions some [illegible]. Why did my State get pooled in with this [illegible] Sect[illegible] you know, so we would have to live with this kind of a [illegible] But [illegible] are some objections to this, and justifiably so, [illegible] think.

DR. [illegible]: There is one point [illegible] that I think [illegible] your making: that is the fact that if one starts by [illegible] number [illegible] correction factors and at any time looks at individual [illegible] records, either average, or particularly individual [illegible] I [illegible] sure your breeders do presently use, you are going [illegible] and seasonal diff[illegible] because these factors do matter, [illegible] and regional differences. The procedure that I have recommended [illegible] Canada does separate [illegible] curves for different seasons and [illegible] actual [illegible] to the average of all cows of [illegible] expr[illegible] perspective [illegible] fairly [illegible] gross [illegible] think [illegible] this [illegible] to [illegible] are looks at actual [illegible] afterwards.

THE CHAIRMAN: [illegible] really [illegible] have but [illegible] quite a bit [illegible] have to [illegible] this out.

DR. [illegible]: Well, the objection that [illegible] valid. There is no question at all that the [illegible] a hard average or anything [illegible] because [illegible] system we have can tend to level out the [illegible] regional fluctuations. This is [illegible] use in getting deviations from [illegible] primarily for [illegible] this purpose.

DR. [illegible]: [illegible] multiplication does it, and if you go the [illegible] way, then [illegible] knock it out.

DR. SMITH: Well, in going the other way [illegible] if we would convert our use to, say, [illegible] and this day we would be multiplying [illegible] would, at least, not [illegible] conversion. We would [illegible] 1.5 to 1.0 instead of 1.0 to 1.35 [illegible]

THE CHAIRMAN: Any comment on this point? It did come up a few times. We are adjusting to a so-called mature equivalent basis now. What about adjusting to a two-year-old basis or something younger?

DR. DICKINSON: There is some merit in that you are adjusting more of the records less. Since the factors will not be completely accurate anyway in all of the situations, you want to adjust records as little as possible.

THE CHAIRMAN: Would it make any difference in estimating breeding values?

DR. HENDERSON: As long as the factors are multiplicative, but operationally, you haven't done anything.

DR. HICKMAN: Wouldn't you reduce the total variance a little bit?

DR. HENDERSON: In sire rank?

DR. HICKMAN: But the sire rank is a different thing. But I mean, total variance is reduced.

DR. FREEMAN: By weight, though. Why would the sire variance stay the same, Dr. Hickman? It has to change because you would be changing the scale.

DR. HICKMAN: The fact is that every time you adjust, you are producing an error; less adjusting -- well, less error.

DR. SMITH: Well, probably one reason for doing this is our most critical proof is the first lactation proof, and these are adjusted the greatest distance now. And if you did it the other way, you would adjust it the least amount.

DR. DICKINSON: One-quarter of our records are first records.

DR. MCGILLIARD: But he is talking about twenty-seven months.

DR. HENDERSON: Why not go from pounds to kilograms? It would accomplish the same thing!

DR. CARTER: I would like to make a comment that I think that we do need to change from our present system. I computed the rank correlation between the New York Curtis bulls, and the Cornell summary and the USDA summary, and it is shocking. I think that part of this is the regional age factor effect. But this tells me that you cannot take bulls used in the region and other bulls used some in that region and mostly in other regions and rank them as accurately as we would like. And this is a real problem for progress in the genetic improvement of dairy cattle if we

can't do this. And part of this is the age factor problem.

THE CHAIRMAN: This situation should be helped by these regional factors.

DR. CARTER: Regionalized, you get this. And then I think if we take that step, we can take a look and see what that does and see whether there is some other factor that is causing this low rank correlation.

DR. HENDERSON: With regard to this matter of whether regional factors will make the mature equivalent record less useful -- I think no more so than before. I thought that we had all more or less come to the thinking that the mature equivalent record was worth very little anyway, so I don't see that you have to compare an ME record all by itself. So what if we do change the magnitude of records by regional factors? Who cares?

DR. PLOWMAN: I think that bull studs and breeders certainly use these. A lot of bull studs won't even look at a cow unless she has got a 20,000 pound record. This is what exists in the industry now. Isn't that right?

MR. BALDWIN: I don't think they look at ME records.

DR. STARKEY: Who provides it for them unless they get it? Where do they look at it? Do they look at ME?

DR. PLOWMAN: Even some of our computing centers are listing records that way and getting records back to dairymen, aren't they? Don't you do that in Iowa?

DR. FREEMAN: The M.E. herdmate average is given over in the right hand corner of the monthly report.

DR. PLOWMAN: And Michigan is doing the same thing, aren't you? On individual cows and deviation records?

DR. CARTER: We use it as a means of arriving at this deviation.

MR. RUMLER: How does a breeder use it?

DR. FREEMAN: Well, I might say that eventually there are going to be some lifetime totals on those sheets on those summary sheets, but that is not really because we thought they were useful.

DR. PLOWMAN: What are you putting them on there for then if they are no good?

can't do this. [illegible] part of this is [illegible] are factor problem.

THE [illegible]: [illegible] this situation about [illegible] helped by these factors.

MR. GARTEN: Regionalized, you get this. And then I think if we take that step, we can take a look and [illegible] if that does and see whether there is some other factor that is causing this low rank correlation.

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DR. [illegible]: M.E. Hardmate [illegible] is given over in the right hand corner of the [illegible] report.

DR. FLOWMAN: [illegible] Michigan is doing the same thing, [illegible] you? Do individual cows [illegible] devi[illegible]ion records?

DR. GARTEN: We use it as a means of arriving at this deviation.

DR. [illegible]: [illegible] a breeder [illegible]?

DR. [illegible]: [illegible] eventually there [illegible] going to be some lifetime [illegible] records [illegible] those sires [illegible] better, but that is [illegible] useful.

[illegible] letting her [illegible] there for th[illegible] if they

DR. FREEMAN: That is a good question to ask.

DR. TOUCHBERRY: I guess the question on some of these things is, what is the purpose of DHIA, isn't it?

DR. MCGILLIARD: DHIA stands for something.

THE CHAIRMAN: Are there any further comments that need to be made on the consideration of dams with primary emphasis on research that may be needed? I realize that one can't put into a few words everything that has happened, but none the less, I think that we want to try to restate some of the problem areas.

DR. BARR: I tried to define one yesterday, but I ran into trouble.

THE CHAIRMAN: Is there work that is needed on contemporary comparisons as a means or possibly a replacement for the herdmate comparison? And, of course, we are thinking of something short of Dr. Henderson's proposal.

DR. LEGATES: Well, I stated that was a need for a little better clarification of how many contemporaries are needed, whether large numbers really are necessary to get what we want in our estimation of breeding values. There is this interaction of sire and herd that comes in, presumably, in the one study of Dr. Allaire's that certainly is a problem that needs to be assessed. I think that we ought to really think seriously about this until Dr. Henderson gets his method worked out, whether we ought to use information that is five and seven years old, putting it together with these bulls that are current. Doing this makes it difficult to really determine what is going on.

I am very much concerned about this, that we shorten the period of the proof or compute a working proof. The big problem is to make immediate decisions of bulls that are available, and I feel that something ought to be done, and I suggest that something along this line is very important operationally.

THE CHAIRMAN: Is there further research that is needed to get a better look at the rank correlations, the comparative rank correlations involved between the herdmate comparison and the contemporary comparison?

DR. LEGATES: I would presume so. As I say, I haven't worked on that. You have got some work here by Dr. Fairchild, and Dr. McDaniel has worked on this also.

DR. HENDERSON: I don't really think that there is much difference between the two procedures. If we had herdmate sires on first lactation records only, then the procedure would be identical except that we are using all records rather than contemporary records. If we go to a contemporary

comparison, we might as well say that we are talking about first records and be done with it. So whether it is herdmate or contemporary doesn't make much difference. I would be in favor of the contemporary procedure, for the reasons that I mentioned this morning, to get around sire - herd correlations.

DR. HICKMAN: There is one thing that I think should be emphasized: That is, the age-time-season interaction for first lactation is greater than it is for any other lactation. And, if you seasonalize overall age correction factors, you are not seasonalizing first lactations as much as they should be -- and this may account for the sire-herd interaction to a large extent.

DR. MCDANIEL: What we have done is to categorize the data by season and region -- I have a sub-class for each season - region combination.

DR. HICKMAN: We are talking about the parity though. You see, the season-age interaction is larger for the first lactation than it is for any other lactation.

DR. FREEMAN: Yes, nobody will argue with that.

DR. HICKMAN: But if you seasonalize the overall age correction factors, you are not going to seasonalize first lactation alone.

DR. MCDANIEL: No, we are not computing these, but I think we should.

DR. PLOWMAN: Different factors for each age and season?

DR. HICKMAN: Well, the yield relationship for first lactation doesn't follow.

DR. HENDERSON: I just took all of these; basically I am getting 21 and 22. And I did this for each calendar month, and then I looked at these and saw what kind of groupings were feasible. It looked to me like a five by seven -- 5-7 grouping would pretty well take care of the situation, so I think that we have done what you are saying.

DR. HICKMAN: Oh, I see. I didn't think that this was the way it was done.

DR. HENDERSON: We conferred about this at some length.

DR. HICKMAN: Certainly herd interaction for first lactation is more confusing than I thought it was.

THE CHAIRMAN: Dr. Henderson also reminded us of the fact that one of the problems with the herdmate comparison is that the assumptions of no genetic trends and correct age adjustment factors are not necessarily valid. In terms of short-time activity in research, is there any additional information we can get in terms of this genetic trend problem?

DR. FREEMAN: Keep them current.

DR. MEADOWS: Just operationally, you mean? Compare bulls of similar age.

DR. FREEMAN: Well, with respect to re-estimating gross age corrections, too, I think. I think this ought to be done reasonably often.

DR. HENDERSON: Well, certainly we get the first lactation ages.

DR. FREEMAN: Yes.

THE CHAIRMAN: I suppose that there are no known adjustments that should be made for this, short of an approach of the type that Dr. Henderson proposed?

DR. HENDERSON: Oh, I suppose one could take a previous estimate of just what this trend is, and this is essentially what one of the things is, and I believe that Dave Harville suggested making correction for this, saying what this trend would be.

DR. LEGATES: If you know what these trends are, and it is consistent in all groups, you know what you are up against.

DR. HENDERSON: Yes, but operationally though, isn't this idea of taking only these daughters that have calved in the last couple of years much more feasible?

DR. FREEMAN: Yes.

DR. HENDERSON: There is nothing to it operationally.

THE CHAIRMAN: Well, our time is really running out, very reluctantly on my part, at least.

Before adjourning, I certainly want to express my very sincere appreciation for all of you being here and the contribution that you have made to this workshop and symposium.

THE CHAIRMAN: Dr. Henderson also reminded us of the fact that one of the problems with the Hermann comparison is that the assumptions of no concrete trends and correct are adjustment factors are not necessarily valid. In terms of short-time activity in research, is there any additional information we can get in terms of this specific trend assumption?

DR. FREEMAN: Keep them current.

DR. CANDOWN: Just operationally, you mean? Compare bulls of similar age.

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DR. HENDERSON: Well, certainly we get the first location soon.

DR. FREEMAN: Yes.

THE CHAIRMAN: I suppose that there are no known adjustments that should be made for this, short of an approach of the type that Dr. Henderson proposed?

DR. HENDERSON: Oh, I suppose one could take a previous estimate of just what this trend is; and this is essentially what one of the things is, and I believe that Dave Harville suggested making correction for that, saying what this trend would be.

DR. LEDERER: If you know what these trends are, and it is consistent in all groups, you know what you are up against.

DR. HENDERSON: Yes, but operationally though, isn't this idea of taking only those daughters that have calves in the last couple of years much more tractable?

DR. [illegible]: Yes.

DR. HENDERSON: There is nothing to it operationally.

THE CHAIRMAN: Well, our time is really running out, very reluctantly on my part. At least.

I rise adjourning. I certainly want to express my very sincere appreciation for all of you being here and the contribution that you have made to this workshop and symposium.

I would especially like to thank the resource people, the speakers, for the job that they have done, and for the contributions that they have made here.

In terms of the USDA sire evaluation program here at Beltsville, I can assure you that this helps us a great deal. We have raised a lot of questions. I think that this was one of our main objectives. And we have certainly answered, I think, quite a few of them. Also, we have provided some good information that should help us to organize our research, thinking of our own work here at Beltsville.